Functional analysis of outer membrane vesicles shed by *Legionella pneumophila*

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“I am not young enough to know everything. “

J. M. Barrie

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1 Summary

The Gram-negative bacterium *Legionella pneumophila* causes Legionnaires' disease, a severe form of pneumonia, in humans. In the environment, the bacterium replicates in amoebae, but it can also infect human phagocytes. The pathogen sheds vesicles from its outer membrane during extracellular and intracellular growth consisting of material from the outer membrane and the periplasm. While the protein composition of *L. pneumophila* OMVs was characterized previously, their role during infections remained elusive.

Biophysical methods were applied to describe their function on the subcellular level. The association of OMVs with membranes *in vitro* was studied using Förster resonance energy transfer and infrared spectroscopy. Both methods revealed the incorporation of OMV components into target membranes with a preference for phosphatidylserine. This integration resulted in a mixed phase composed of bacterial and host lipids with a higher phase transition temperature, i.e. a lower fluidity than the initial liposomes. Fusions of *L. pneumophila* OMVs and host membranes potentially deliver bacterial factors into the host cell and into the target membrane itself.

The role of *L. pneumophila* OMVs during infections was further elucidated with a novel infection model comprising living human lung tissue. In contrast to current models, it contains all cell types and extracellular components of the human lung, thus mirroring the organ-specific situation *in vivo*. *L. pneumophila* replicated within host cells and could be detected on the entire alveolar lining as well as on and in alveolar macrophages, while OMVs specifically localize to macrophages. The model sheds light on the specific damage to pulmonary tissue components, including connective tissue fibers and alveolar epithelia. Moreover, it allows for the molecular characterization of infection by analyzing the transcriptome of the infected tissue, thereby identifying the proteins uteroglobin and MARCO as potential new host factors involved in *L. pneumophila* virulence.

The results from this work reveal new aspects about the interactions between *L. pneumophila* and its human host as well as the mechanism of OMV fusion. The lung explant infection model will enable to identify new virulence factors and host components crucial in *L. pneumophila* infections.

2 Zusammenfassung

Das Gram-negative Bakterium *Legionella pneumophila* verursacht beim Menschen die Legionärskrankheit, eine schwere Form der Lungenentzündung. In der Umwelt repliziert das Bakterium in Amöben, kann allerdings auch menschliche Phagozyten infizieren. Das Pathogen schnürt während extra- und intrazellulärem Wachstum Vesikel von seiner Oberfläche ab, die aus Komponenten der äußeren Membran und des Periplasmas bestehen. Die Proteinzusammensetzung von *L. pneumophila*-OMVs wurde bereits untersucht, ihre Rolle während einer Infektion ist allerdings unbekannt.

Mit Hilfe biophysikalischer Methoden wurde ihre subzelluläre Funktion untersucht. Förster-Resonanzenergietransfer- und Infrarotspektroskopie zeigten den Einbau von OMV-Komponenten in Zielmembranen *in vitro*, wobei Phosphatidylserin-haltige Membranen bevorzugt wurden. Aus dieser Integration resultierte eine gemischte Phase aus Lipiden des Bakteriums und des Wirts mit einer höheren Phasenübergangstemperatur, d.h. Fluidität, als die Ausgangsliposomen. Die Fusion von *L. pneumophila*-OMVs und Wirtsmembranen führt potenziell zur Ausschüttung bakterieller Faktoren in die Wirtszelle oder die Zielmembran selbst.

Die Rolle von *L. pneumophila*-OMVs während Infektionen wurde mit einem neuartigen Infektionsmodell aus lebendem menschlichem Lungengewebe weitergehend untersucht. Im Gegensatz zu bisherigen Modellen beinhaltet dieses alle Zelltypen und extrazellulären Komponenten der menschlichen Lunge und spiegelt so die Situation während einer Infektion *in vivo* wider. *L. pneumophila* replizierte in Wirtszellen und konnte an der gesamten Alveolaroberfläche sowie in und an Alveolarmakrophagen detektiert werden, wohingegen OMVs spezifisch an Makrophagen lokalisierten. Das Modell wies nach Infektion mit *L. pneumophila* weiterhin spezifische Schäden an Lungengewebskomponenten auf, darunter Bindegewebsfasern und Alveolarepithelien. Darüber hinaus erlaubt es die molekulare Charakterisierung der Infektion durch Analyse des Transkriptoms des infizierten Gewebes, wodurch Uteroglobin und MARCO als potenzielle Wirtsfaktoren identifiziert wurden, die an *L. pneumophila*-Infektionen beteiligt sind.

Die Ergebnisse dieser Arbeit zeigen neue Aspekte der Interaktionen zwischen *L. pneumophila* und seinem menschlichen Wirt und den Mechanismus der Fusion von OMVs. Mit Hilfe des Infektionsmodells mit Lungengewebe können neue Virulenzfaktoren sowie Wirtsproteine identifiziert werden, die wichtige Rollen während Infektionen mit *L. pneumophila* spielen.

3 Introduction

3.1 *Legionella pneumophila:* physiology and virulence

The pathogen *Legionella pneumophila* is the most important species of the over 60 members of the family Legionellaceae, causing over 70 % of human *Legionella* infections (Joseph, 2004; DSMZ, 2013). The family Legionellaceae can be divided in 70 serogroups, of which serogroup 1 leads to over 60 % of reported infections (Marston *et al.*, 1994). It is the main causative agent of Legionnaires' disease, which will be discussed in chapter 3.3.

L. pneumophila is a Gram-negative, obligate aerobic, rod-shaped γ-proteobacterium with one flagellum and a temperature optimum between 25 and 37 °C (Figure 1). The average cell length is 2 µm, but the shape of the bacterium varies depending on culture conditions (Katz *et al.*, 1984). Iron and amino acids are critical nutrients for the bacterium (Reeves *et al.*, 1981; Eylert *et al.*, 2010).

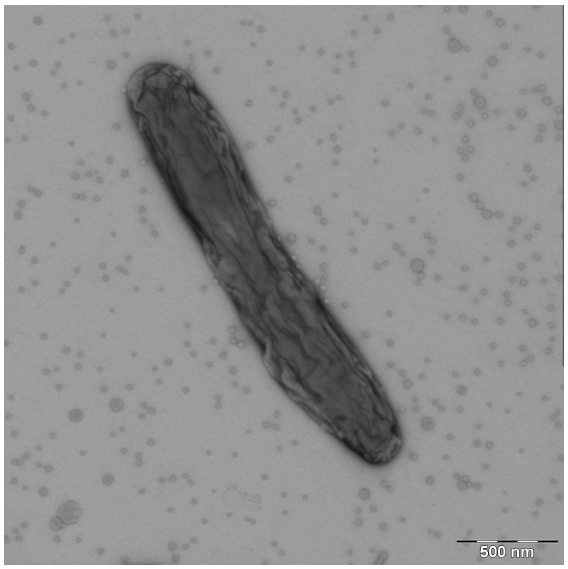

Figure 1. Electron micrograph of *L. pneumophila* (Jana Tiefenau/Manfred Rohde).

The membrane composition of *L. pneumophila* is distinctly different from that of most other bacteria. Besides phosphatidylethanolamine, phosphatidylglycerol and cardiolipin, the pathogen contains phosphatidylcholine as the major phospholipid of its membranes (Finnerty *et al.*, 1979). This molecule is found predominantly in eukaryotes and in approximately 10 % of all described bacterial species, usually those who are pathogenic or live in close association with eukaryotes (Sohlenkamp *et al.*, 2003). In the case of *L. pneumophila*, a decrease in phosphatidylcholine

negatively influences several virulence traits (Conover *et al.*, 2008). Also, exceptionally many *L. pneumophila* phospholipid molecules are bound to branched-chain fatty acids, increasing the resistance to antimicrobial peptides (Verdon *et al.*, 2011). In addition, the hydroxyl groups of the O-antigen of *L. pneumophila* lipopolysaccharide (LPS) molecules are acetylated, resulting in a hydrophobic cell surface (Knirel *et al.*, 1994).

The natural habitats of *L. pneumophila* are freshwaters and moist soils, where it lives planctonically, associated with biofilms or within protozoa. Biofilms and physiological adaptations protect the bacterium from harmful stimuli such as antibiotics or other hazardous chemicals (Rogers *et al.*, 1992; Alleron *et al.*, 2008). In addition, biofilms attract protozoa which prey on bacteria. *L. pneumophila*, however, replicates within amoebae or other phagocytes as a facultative intracellular pathogen (Rowbotham, 1980b; Murga *et al.*, 2001). Life within host cells protects *L. pneumophila* from exogenous hazards and provides the required nutrients (Rowbotham, 1980b; Fields, 1996).

Besides environmental sources, *L. pneumophila* can also be detected in technical devices containing warm water, such as showers, pools, air conditioning systems and cooling towers (Garcia *et al.*, 2013; Lau *et al.*, 2013; Serrano-Suarez *et al.*, 2013). Contaminated aerosols can transfer the bacterium from these so-called technical vectors into the mammalian respiratory tract. There, *L. pneumophila* can invade and replicate within alveolar macrophages, epithelial cells and even endothelial cells (Winn *et al.*, 1981; Mody *et al.*, 1993; Chiaraviglio *et al.*, 2008). Events regarding *L. pneumophila* pathogenicity are closely related in infected amoebae and mammalian cells. Crucial components and mechanisms of endosomal trafficking are very similar in professional phagocytes (Fields, 1996; Steinert *et al.*, 2002).

3.2 Intracellular life cycle

3.2.1 Adhesion and uptake

The life cycle of *L. pneumophila* in protozoan or mammalian host cells, from uptake to release, lasts approximately 24 h (Figure 2). Several outer membrane proteins are involved in the adhesion of *L. pneumophila* to its host cells, among them MOMP, the major outer membrane protein, and Hsp60 (Bellinger-Kawahara *et al.*, 1990; Garduno *et al.*, 1998). On mammalian cells, complement receptors CR1 and CR3

serve as binding sites for the pathogen (Payne *et al.*, 1987), while E-cadherin and integrins are involved in *L. pneumophila* adhesion to lung epithelial cells (Prashar *et al.*, 2012). Attachment to the cell surface of amoebae is partially mediated by interactions between bacterial oligosaccharides and amoebal lectins (Declerck *et al.*, 2007). The bacterium is taken up by coiling or conventional phagocytosis into the so-called *Legionella*-containing vacuole (LCV), whose protein composition it modifies immediately after entry (Horwitz, 1983; Horwitz, 1984; Bitar *et al.*, 2004; Tachado *et al.*, 2008; Harada *et al.*, 2012).

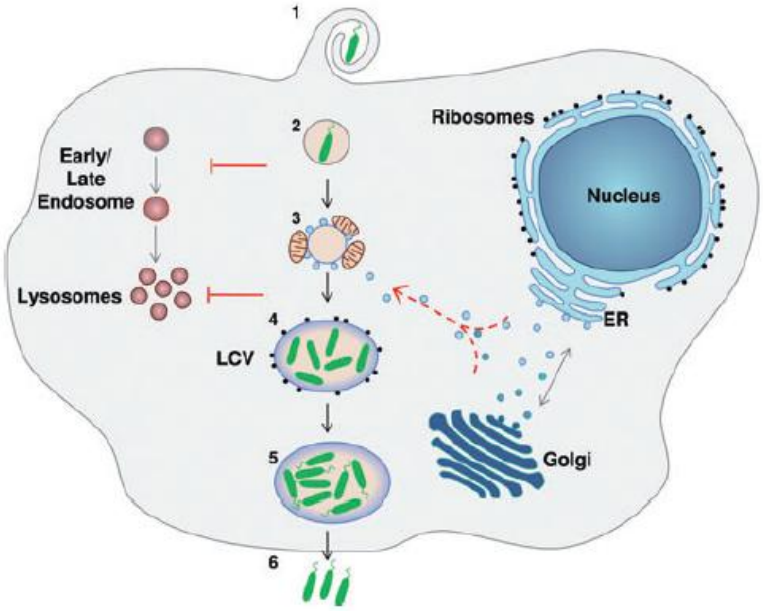

Figure 2: Intracellular life cycle of *L. pneumophila* in protozoa or mammalian host cells; modified from (Franco *et al.*, 2009). The pathogen is taken up by the eukaryotic host cell via conventional or coiling phagocytosis (1). Immediately after entry, the *Legionella*-containing vacuole (LCV) avoids fusion with lysosomes (2). Within the first hour, the LCV associates with mitochondria and interferes with the early secretory pathway by recruiting ER-derived vesicles trafficking to the Golgi which fuse with the vacuole (3). A rough ER-like replicative vacuole surrounded with ribosomes is formed (4) and in this remodeled phagosome bacteria undergo several rounds of replication, become flagellated (5) and ultimately escape the host and start a new infection cycle in neighboring cells (6).

3.2.2 Modification of the *Legionella*-containing vacuole by secreted proteins

Within minutes after phagocytosis, ER vesicles fuse with the LCV mediated by SNARE proteins (Robinson *et al.*, 2006; Arasaki *et al.*, 2010). Mitochondria are also recruited to the LCV in the first hours after uptake, followed by ribosomes (Horwitz,

1983; Abu Kwaik, 1996; Kagan *et al.*, 2002; Derre *et al.*, 2004; Robinson *et al.*, 2006) (Figure 3).

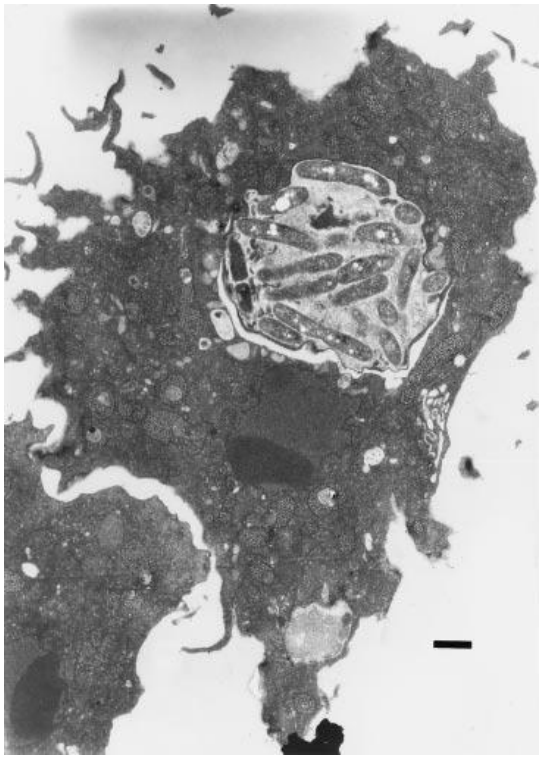

Figure 3: *L. pneumophila* cells in a *D. discoideum* cell (Hägele *et al.*, 2000). Bar = 1 µm.

The key feature of *L. pneumophila* virulence is the prevention of the fusion of the LCV with lysosomes. It is accomplished by the secretion of a large number of effector proteins into the host cytosol via a type IVB secretion system termed Dot/Icm, an abbreviation for “Defective organelle trafficking/Intracellular multiplication” (Ensminger *et al.*, 2009; Franco *et al.*, 2009; Hubber *et al.*, 2010). These effectors manipulate the host cell in many sophisticated ways.

An example of such an effector is DrrA, a protein which is anchored to the LCV membrane after type IVB secretion (Machner *et al.*, 2006; Murata *et al.*, 2006). It recruits Rab1, a GTP-hydrolyzing host protein, which is a key component of the eukaryotic membrane cycling machinery (Zerial *et al.*, 2001). Rab1 is particularly important for the fusion between ER-derived vesicles and the Golgi apparatus and can recruit Sec22b to the LCV membrane, a protein on ER-derived vesicles which is essential for this fusion (Hay *et al.*, 1997; Moyer *et al.*, 2001; Kagan *et al.*, 2004). Thus, the Dot/Icm-dependent secretion of DrrA leads to the recruitment and fusion of ER-derived vesicles with the LCV, significantly contributing to the intracellular survival and replication of *L. pneumophila* (Arasaki *et al.*, 2012).

The intracellular replication of *L. pneumophila* starts approximately eight hours after infection. The pathogen acquires nutrients from the host cell, in particular amino acids. The Dot/Icm effector AnkB plays an important role in this step. This protein is secreted into the host cytosol, where it is farnesylated by host enzymes to be anchored on the cytosolic face of the LCV membrane (Price *et al.*, 2010). There, AnkB recruits high amounts of polyubiquinated proteins (Price *et al.*, 2009). Intriguingly, these proteins are degraded by the proteasome, thereby supplying amino acids for the carbon and energy metabolism of *L. pneumophila* (Eylert *et al.*, 2010; Price *et al.*, 2011). This function of AnkB is indispensable for the intracellular replication of the pathogen (Price *et al.*, 2010).

Similarly, SidK is secreted into the host cell to inhibit the function of a vacuolar H^+-ATPase directly in order to prevent the acidification of the LCV (Xu *et al.*, 2010). The importance of a neutral pH inside the LCV in later infection stages is disputed since an acidification does not appear to abolish the replication of *L. pneumophila* and the progression of infection (Sturgill-Koszycki *et al.*, 2000; Wieland *et al.*, 2004). It is discussed that LCV acidification may act as a signal to initiate release from the LCV and subsequently from the host cell itself (Sturgill-Koszycki *et al.*, 2000).

In addition to the type IVB secretion system, *L. pneumophila* also features a type II secretion system which translocates over 25 proteins into the surrounding medium, including various enzymes (Cianciotto, 2009). This secretion system is required for successful replication within amoeba and extracellular growth at low temperatures and contributes to replication within mammalian host cells and the infection of mice and guinea pigs (Hales *et al.*, 1999; Liles *et al.*, 1999; Rossier *et al.*, 2004; DebRoy *et al.*, 2006). The major secretory protein, a zinc-dependent metalloprotease termed ProA, is the most abundant protein in *L. pneumophila* culture supernatants and is secreted via the type II secretion system (Hales *et al.*, 1999).

Furthermore, the genome of several *L. pneumophila* strains contains genes putatively coding for components of a type I secretion system (Jacobi *et al.*, 2003). A type IVA secretion system can be detected predominantly in *L. pneumophila* patient isolates, which suggests a role in virulence (Segal *et al.*, 1999; Samrakandi *et al.*, 2002). Some strains also feature type V secretion systems with a currently unknown role in virulence (Cazalet *et al.*, 2004). For secretion systems of types I, IVA and V, no substrates have been characterized so far.

3.2.3 Release from the LCV and the host cell

When the nutrients of the host cell are depleted, the pathogen stops replicating and initiates processes to escape from the LCV and subsequently from the host cell to infect neighboring cells. After this differentiation process, *L. pneumophila* is highly stress-resistant and motile (Molofsky *et al.*, 2004). An electron microscopy-based study suggests that at this point, the pathogen disrupts the LCV membrane and moves freely throughout the host cytoplasm (Molmeret *et al.*, 2004). Later, after pore formation in the host cell and subsequent cell death, *L. pneumophila* can escape and infect other cells (Kirby *et al.*, 1998; Molmeret *et al.*, 2002). The exact mode of host cell death is still disputed; apoptosis, necrosis and pyroptosis are considered (Kirby *et al.*, 1998; Morinaga *et al.*, 2010; Maeda *et al.*, 2011; Katagiri *et al.*, 2012). The induction or inhibition of the individual cell death mechanisms is thought to depend on the stage of infection and on the specific conditions.

Importantly, the differentiation from a replicative phase to a transmissive phase is mirrored during the cultivation of *L. pneumophila* under laboratory conditions. The gene expression profile and proteome of the pathogen in the first hours after uptake, when it synthesizes proteins involved in carbohydrate and amino acid metabolism, resemble those of cultures in the exponential growth phase. The nutrient-depleted transmissive stage is represented by post-exponential cultures, in which the bacterium expresses virulence-related genes such as flagella subunits and type IVB secretion substrates (Hammer *et al.*, 2002; Molofsky *et al.*, 2004; Brüggemann *et al.*, 2006; Dalebroux *et al.*, 2009; Hayashi *et al.*, 2010).

3.3 Legionnaires' disease and Pontiac fever

After the inhalation of *Legionella*-contaminated aerosols and the establishment of the intracellular replication niche in pulmonary host cells, an atypical form of bacterial pneumonia can arise. The first recorded outbreak of Legionnaires' disease occurred among the participants of a meeting of the American Legion in Philadelphia in 1976, resulting in 182 infections and 29 deaths (Fraser *et al.*, 1977). This prototypic epidemic led to the discovery of the pathogen as well as the naming of the disease and its causative agent (Fraser *et al.*, 1977; McDade *et al.*, 1977). The mortality rate of Legionnaires' disease is about 20 %. In Germany, approximately 20,000 cases

occur per year, while only a small fraction is diagnosed and reported to the authorities. Senior citizens, smokers and persons with a compromised immune system have the highest risk to contract Legionnaires' disease (von Baum *et al.*, 2008).

The current knowledge about the pathology of Legionnaires' disease was drawn from histological studies on autopsy material from patients who died from the disease (Winn *et al.*, 1981). In affected alveoli, a massive infiltration of neutrophils and macrophages can be observed. The architecture of the lung tissue appears disrupted, alveolar epithelia are detached from the connective tissue and a protein-rich exudate can be detected in the alveoli (Glavin *et al.*, 1979). The structural damage to the tissue allows the infection to spread to neighboring alveoli and lobes of the lung. In late infection stages, *L. pneumophila* breaks the endothelial barrier and disseminates to the spleen, kidneys, bone marrow and lymph nodes via the bloodstream (Watts *et al.*, 1980; Hambleton *et al.*, 1982; Theaker *et al.*, 1987).

A second form of legionellosis is called Pontiac fever. It presents itself as an influenza-like, self-limiting disease lasting up to six days; however there is no exact definition of the disease (Glick *et al.*, 1978; Edelstein, 2007). It is unclear why infections with the same pathogen can lead to two clinical pictures. Soluble endotoxin, a low number of infecting bacteria and interplay between bacterial and protozoan factors are discussed to mediate Pontiac fever pathogenesis (Blaser, 1977; Rowbotham, 1980a; Fields *et al.*, 2001; Edelstein, 2007). Due to the mild course of infection and the ambiguous definition of Pontiac fever, the number of cases is unknown.

Human-to-human transmission of *L. pneumophila* in Legionnaires' disease or Pontiac fever has never been described, so humans are not considered a natural host for *Legionella* species. Both types of legionellosis can also be caused by other species of the genus *Legionella*, such as *L. longbeachae* or *L. oakridgensis* (Lo Presti *et al.*, 2000; Cramp *et al.*, 2010).

3.3.1 Host response to *L. pneumophila* infections

The immune response to an infection with *L. pneumophila* is characterized by the synthesis and/or secretion of cytokines like IL-1α, pro-IL1β, IL-6, IL-8, IL-12, CXCL1, TNF-α and IL-17 (Teruya *et al.*, 2007; Shin *et al.*, 2008; Kimizuka *et al.*, 2012). This

response has been studied most thoroughly in murine macrophages, where the cytokine secretion exclusively depends on signaling downstream of Toll-like receptor 2 (Akamine *et al.*, 2005; Shin *et al.*, 2008; Shim *et al.*, 2009). TLR2 is activated by lipopolysaccharides (LPS) from *L. pneumophila*, even though LPS molecules usually stimulate TLR4-dependent responses (Girard *et al.*, 2003). *L. pneumophila* shares this uncommon feature with other pathogens such as *Rhizobium, Bacteroides, Chlamydia* and *Pseudomonas* species (Girard *et al.*, 2003; Erridge *et al.*, 2004). IL-8 synthesis by alveolar epithelial cells is mediated by *L. pneumophila* flagellin and a functional Dot/Icm secretion system (Frutuoso *et al.*, 2010). The epithelial production and secretion of IL-6 and TNF-α depends on the invasion of *L. pneumophila* and not only its contact with the host cell surface (Chang *et al.*, 2004). Importantly, there seem to be considerable differences between individual hosts, since e.g. neutrophils from only 40 % of donors secreted CXCL7 after stimulation with *L. pneumophila* (Gonzalez-Cortes *et al.*, 2012). The overall cytokine response of infected macrophages and epithelial cells is weakened by type II secretion system substrates (McCoy-Simandle *et al.*, 2011).

In a recent study, the transcriptional profile of *L. pneumophila*-infected mouse lungs was compared to the response to infections with *P. aeruginosa, Yersinia pestis* and *Francisella tularensis* (Walters *et al.*, 2013). Among these pathogens, *L. pneumophila* caused an inflammatory response of intermediate intensity with a particularly high number of downregulated genes or genes without differential expression in the first 48 h after infection. However, *L. pneumophila* only causes a self-limiting infection in the mouse strain used in this study (see chapter 3.5).

Apart from cytokine responses, serum levels of hepatocyte growth factor (HGF) are significantly increased in patients with Legionnaires' disease compared to other bacterial pneumonias or tuberculosis. Higher levels of HGF correlate with a higher mortality rate. Additionally, serum lactate dehydrogenase levels are increased in Legionnaires' disease patients as a result of cellular and tissue destruction (Higa *et al.*, 2011).

Besides cytokine responses, several cell types are involved in *L. pneumophila* infections. Alveolar macrophages and alveolar epithelial cells are the most common host cells exploited for intracellular replication by the pathogen. Affected cells employ mechanisms to limit and terminate the infection, including pyroptosis mediated by

caspases 1 and 11 (Miao *et al.*, 2010; Aachoui *et al.*, 2013; Case *et al.*, 2013). Many other cellular defense mechanisms are modified by *L. pneumophila*, including autophagy and the formation of reactive oxygen species (Harada *et al.*, 2007; Choy *et al.*, 2012). The activation of T-cells is inhibited by *L. pneumophila* by down-regulating the expression of stimulatory MHC class I molecules in infected cells (Neumeister *et al.*, 2005).

Neutrophils are present in affected alveoli of Legionnaires' disease patients in great numbers (Winn *et al.*, 1981), but their contribution to disease progression is unclear. For the recruitment of these cells to *L. pneumophila*-affected alveoli, Nod-like receptors and IL-17 are reported to be required (Frutuoso *et al.*, 2010; Kimizuka *et al.*, 2012). In contrast to uptake by macrophages, *L. pneumophila* must be opsonized to invade neutrophils and subsequently evades killing by inhibiting the oxidative burst (Verbrugh *et al.*, 1985; Rechnitzer *et al.*, 1987).

3.4 Bacterial outer membrane vesicles

To export complexes of proteins, lipids and membrane-associated molecules, Gram-negative bacteria shed outer membrane vesicles (OMVs) from their outer membrane. The first reports on so-called "pinched-off membrane sacs" originate from the 1960s, when electron micrographs showed vesicles on the surface of *Vibrio cholerae* cells (Chatterjee *et al.*, 1967). The production of OMVs has been described for a plethora of Gram-negative bacteria, including human pathogenic species (Schertzer *et al.*, 2013). Some Gram-positive bacteria also shed vesicles from their membrane (Lee *et al.*, 2009).

The diameter of OMVs ranges from 50 to 250 nm (Beveridge, 1999). They consist of the major components of the outer membrane, namely lipopolysaccharides and phospholipids, as well as proteins derived from the outer membrane and the periplasmic space. The proteomes of OMVs from different species, including *L. pneumophila*, have been studied in recent years (Galka *et al.*, 2008; Lee *et al.*, 2009; Kahnt *et al.*, 2010; Choi *et al.*, 2011). Lipid and LPS analyses of OMVs are rarer, but together with proteomic studies revealed that the relative abundances of OMV components differ from that of the outer membrane, indicating a regulated sorting process (Kadurugamuwa *et al.*, 1995; Horstman *et al.*, 2000; Kato *et al.*,

2002; Fernandez-Moreira *et al.*, 2006; Bomberger *et al.*, 2009; Tashiro *et al.*, 2011). For *Porphyromonas gingivalis*, a cargo sorting process was hypothesized which preferentially includes virulence-related proteins into OMVs, depending on the presence of high molecular weight LPS (Haurat *et al.*, 2011).

Much less is known about the formation of OMVs (Figure 4). It was shown that the lipophilic *P. aeruginosa* quorum sensing molecule PQS is not only contained in OMVs, but that the molecule also interacts with membranes composed of phospholipids or *P. aeruginosa* LPS (Mashburn *et al.*, 2005; Mashburn-Warren *et al.*, 2008). This incorporation is thought to provide the membrane curvature necessary for the shedding of vesicles from the outer membrane. However, this mechanism seems to be unique to *P. aeruginosa* (Mashburn-Warren *et al.*, 2008). In *Escherichia coli*, proteins involved in the synthesis and modification of peptidoglycan and outer membrane components were shown to influence OMV production quantitatively, but these changes may result from the pleiotropic effects of the mutations (McBroom *et al.*, 2006). A general mechanism of OMV formation has not been described comprehensively yet.

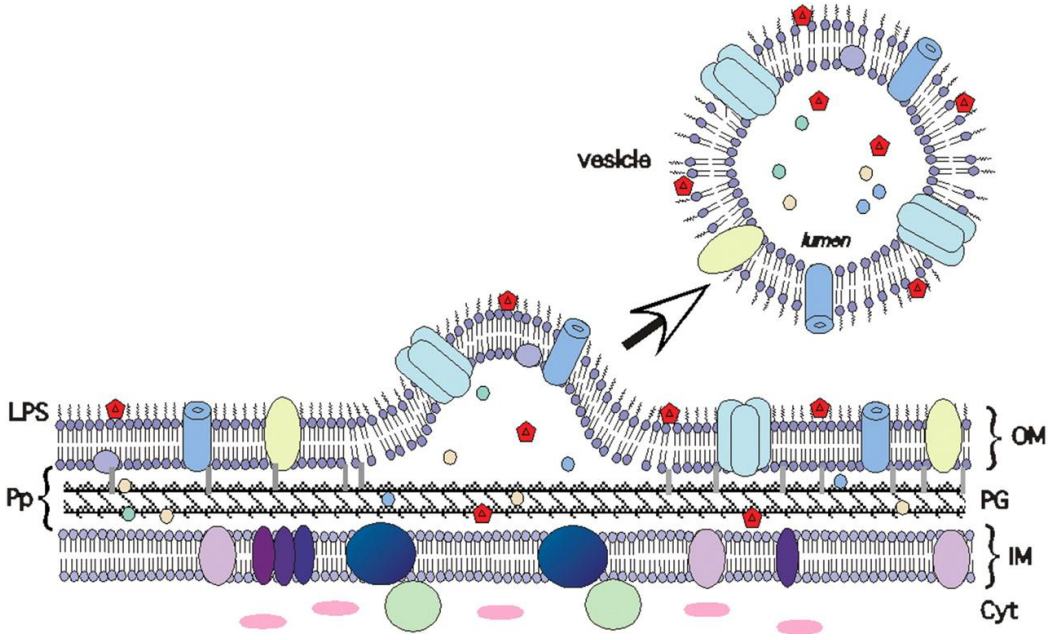

Figure 4: Model of OMV biogenesis; (Kuehn *et al.*, 2005). OM vesicles are proteoliposomes consisting of OM phospholipids and LPS, a subset of OM proteins, and periplasmic (luminal) proteins. Proteins (red) that adhere to the external surface of the bacteria are associated with the external surface of vesicles. Proteins and lipids of the IM and cytosolic content are excluded from OM vesicles. (LPS) Lipopolysaccharide; (Pp) periplasm; (OM) outer membrane; (PG) peptidoglycan; (IM) inner membrane; (Cyt) cytosol.

3.4.1 Functions of bacterial OMVs

Bacterial OMVs have been implicated in many functions, all of them comprising communication with other prokaryotes or eukaryotes.

The OMVs of some bacteria, including *P. aeruginosa*, have been shown to kill other bacterial species effectively (Li *et al.*, 1998). This killing is, at least in part, due to autolysins exported via OMVs, which are thought to fuse with the outer membrane of the respective target microorganism (Li *et al.*, 1996; Li *et al.*, 1998). The bactericidal activity of *P. aeruginosa* OMVs was increased if the antibiotic gentamicin was added to the cultures. This molecule was packaged into OMVs to be exported from the periplasm, indicating a protective function of OMVs against exogenous harmful stimuli (Kadurugamuwa *et al.*, 1995; Kadurugamuwa *et al.*, 1996). This is underlined by the finding that a *Pseudomonas putida* strain eliminates toluene, which adhered to the bacterial surface, via membrane vesicles with a particularly low protein content (Kobayashi *et al.*, 2000). In addition to stimulation with antibiotics and organic solvents, OMVs are also considered a part of the response against oxidative stress and peptidoglycan damage in *P. aeruginosa* (Macdonald *et al.*, 2013).

OMVs are reported to be an extracellular component of biofilms, where they are found both detached and tethered to bacterial surfaces (Beveridge *et al.*, 1997; Schooling *et al.*, 2006; Palsdottir *et al.*, 2009). *P. gingivalis* OMVs promote adhesion between two other bacteria in the same habitat, indicating a role in biofilm formation (Grenier, 2013). For *Helicobacter pylori*, the formation of biofilms depends on the presence of an OMV-specific protein (Yonezawa *et al.*, 2011).

Some studies show that OMVs can contain RNA and DNA which can transform other microorganisms (Kadurugamuwa *et al.*, 1995; Kolling *et al.*, 1999; Rumbo *et al.*, 2011). The adhesion between bacterial cells or between pathogens and their host cells can also be modified by OMVs (Kamaguchi *et al.*, 2003; Inagaki *et al.*, 2006; Pollak *et al.*, 2012).

With regard to host-pathogen interactions, OMVs have been found to play a multitude of roles. For several species, OMVs have been reported to be enriched in virulence-related proteins, which can be delivered to host cells over long distances (Galka *et al.*, 2008; Bomberger *et al.*, 2009; Haurat *et al.*, 2011). Due to the small size of the vesicles, they are thought to diffuse more rapidly and farther than a bacterial cell

could migrate. They are thus hypothesized to affect distant host cells, e.g. by eliciting secretory responses or by priming cells for later invasion.

Once arrived at a host cell, the OMV cargo can be delivered. The exact mechanism of this process has not been clarified in all cases; however, adhesion to mammalian cells is observed for OMVs of *P. gingivalis*, *P. aeruginosa* and *E. coli* (Tsuda *et al.*, 2008; Bauman *et al.*, 2009; Furuta *et al.*, 2009b; Kim *et al.*, 2013).

After adhesion and subsequent internalization, *P. aeruginosa* OMV components are localized in the endoplasmic reticulum (Bauman *et al.*, 2009). Vesicles from this pathogen are also suggested to fuse with host cell lipid rafts to release several virulence factors from their lumen into the cytosol (Bomberger *et al.*, 2009). *P. gingivalis* OMVs also enter epithelial cells at lipid rafts, but are transported to lysosomes (Tsuda *et al.*, 2008; Furuta *et al.*, 2009b). Proteins in and on OMVs from this pathogen interfere with host cell migration, proliferation and iron metabolism (Furuta *et al.*, 2009a).

The role of bacterial OMVs in infections on the tissue level is poorly described. OMVs derived from *E. coli* were shown to induce the synthesis of adhesion molecules by pulmonary endothelia, the adhesion of leukocytes and the extravasation of neutrophils into the alveolar lumen (Kim *et al.*, 2013). *Acinetobacter baumannii* OMVs are shed from the bacterial surface in murine lungs and may contribute to the observed tissue damage including hemorrhage and neutrophil infiltration (Jin *et al.*, 2011).

OMVs are reported to modulate the immune response differently than the bacterium itself during infections with *P. gingivalis* (Nakao *et al.*, 2011), *Brucella abortus* (Pollak *et al.*, 2012), *Neisseria meningitidis* (Lee *et al.*, 2007), *Moraxella catarrhalis* (Schaar *et al.*, 2011) and also *L. pneumophila* (Galka *et al.*, 2008), as shown by studies on the cytokine profiles of infected cells *in vitro*. Both protein and LPS molecules are involved in this process (Ellis *et al.*, 2010). Vesicles from *P. aeruginosa* were shown to cause an inflammatory reaction in murine lungs which is similar to the response to whole *P. aeruginosa* cells (Park *et al.*, 2013). Additionally, OMVs are thought to protect some pathogens against bactericidal components of human serum, firstly because they act as decoys to bind the aforementioned molecules, and secondly because they contain proteases which can cleave immunoglobulins and complement

proteins. This was demonstrated for OMVs shed by *P. gingivalis* (Grenier *et al.*, 1991).

The immunomodulatory role of OMVs has been exploited to engineer vesicle-based vaccines against infections with *A. baumannii* (McConnell *et al.*, 2011), *P. gingivalis* (Nakao *et al.*, 2011) and even the eukaryotic pathogen *Leishmania donovani* (Schroeder *et al.*, 2009). This approach is already widely applied to prevent infections with *N. meningitidis* by injecting vesicles with lower LPS content or a modified protein composition (van der Ley *et al.*, 2011; van de Waterbeemd *et al.*, 2012; van de Waterbeemd *et al.*, 2013). Moreover, there are studies indicating that *N. meningitidis* OMVs are a potent adjuvant for a potential vaccine against HIV (Aghasadeghi *et al.*, 2011). However, vesicle-based vaccinations have to be monitored carefully since OMVs alone have been shown to cause sepsis in rat and mouse infection models (Park *et al.*, 2010; Shah *et al.*, 2012).

3.4.2 *L. pneumophila* OMVs

OMVs from *L. pneumophila* were depicted on early electron micrographs of the bacterium, but disregarded as “condensed pili-related proteins or random structural proteins of the outer membranes” (Rodgers *et al.*, 1982). They have only been studied in recent years. *L. pneumophila* produces OMVs in all growth phases as well as during intracellular infections (Figure 5, (Galka *et al.*, 2008)). They contain 74 different proteins, 33 of which are OMV-specific. Virulence-related proteins such as MOMP, Hsp60 and Mip are overrepresented, thus a role during pathogenesis is likely. *L. pneumophila* OMVs exhibit proteolytic and lipolytic enzyme activities.

Moreover, *L. pneumophila* OMVs increase the metabolic activity of *Acanthamoeba castellanii*, suggesting a role in amoebal nutrition (Galka *et al.*, 2008), and do not change the viability of macrophages (Fernandez-Moreira *et al.*, 2006; Jäger *et al.*, 2013a). The cytokine response of alveolar epithelial cells is altered after exposure to OMVs, resulting in an increased secretion of IL-6, IL-7, IL-8, IL-13, granulocyte colony-stimulating factor, IFN-γ, and monocyte chemoattractant protein 1 (MCP-1). IL-7 and IL-13 are induced specifically compared to stimulation with *L. pneumophila* cells (Galka *et al.*, 2008).

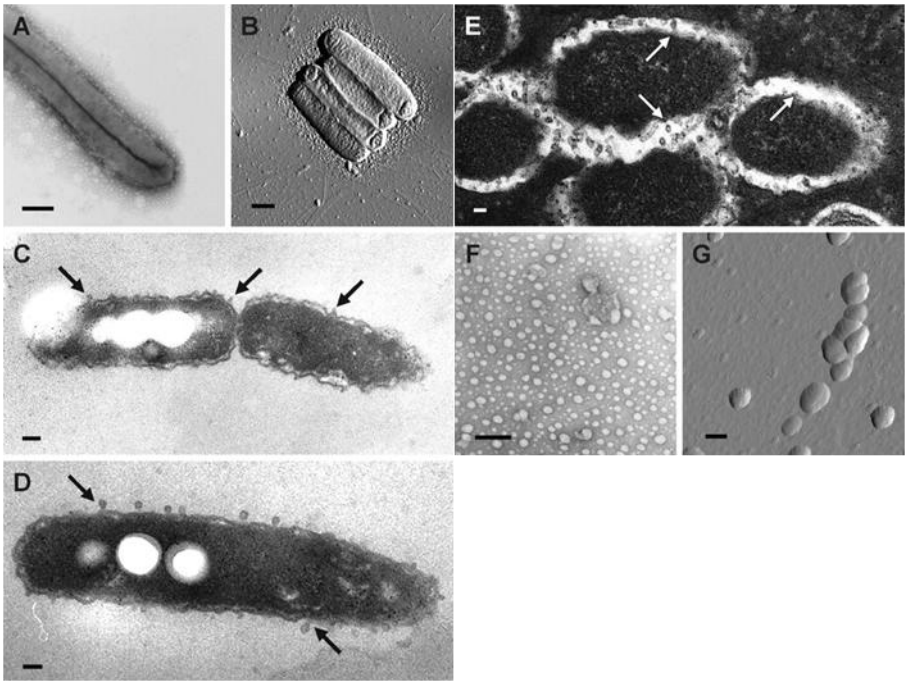

Figure 5: *L. pneumophila* secretes OMVs under extra- and intracellular conditions; modified from (Galka *et al.*, 2008). (A and B) Secretion of OMVs by *L.pneumophila* grown on solid medium. Bars = 0.5 µm. (C and D) Production of OMVs by *L. pneumophila* during the logarithmic phase (C) and stationary phase (D) of extracellular growth. Arrows indicate OMVs budding off the membrane surface. Bars = 0.5 µm (C) and 0.2 µm (D). (E) OMV production by *L. pneumophila* in LCVs of infected *D. discoideum* host cells. The arrows indicate OMV budding sites on the membrane surface. Bar = 0.2 µm. (F and G) OMVs purified from bacterial liquid cultures. Bars = 0.2 µm.

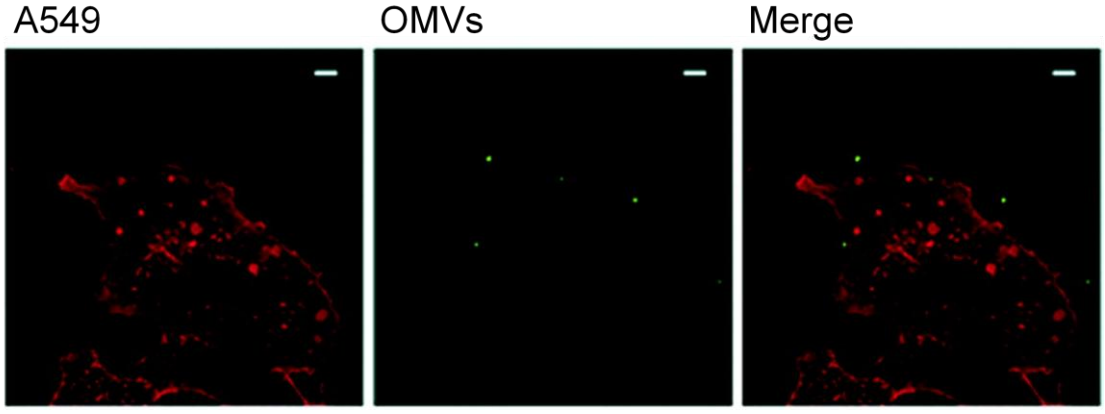

Figure 6: Confocal laser-scanning microscopy images of the binding of *L. pneumophila* OMVs to host cell membranes; modified from (Galka *et al.*, 2008). A549 alveolar epithelial cells (red) were incubated with 25 µg of OMVs (green) for 8 h. Bars = 5 µm.

On the cellular level, *L. pneumophila* OMVs are shown to associate with the surface of alveolar epithelial cells *in vitro* (Figure 6, (Galka *et al.*, 2008)). Importantly, they are sufficient to inhibit the fusion of phagosomes with lysosomes after uptake by macrophages. This inhibition is at least partially mediated by LPS molecules on

OMVs, which are regulated differentially depending on the growth phase (Fernandez-Moreira *et al.*, 2006; Seeger *et al.*, 2010). The latter finding indicates a role for OMVs in the differentiation from the transmissive to the replicative phenotype during intracellular infection, since outer membrane material is shed and new surface proteins can be displayed (Fernandez-Moreira *et al.*, 2006).

3.5 Model systems to study *L. pneumophila* infections

Many different experimental models have been established to analyze specific aspects of infections with *L. pneumophila*. Besides human monocellular systems like macrophages and epithelial cells (Pearlman *et al.*, 1988; Mody *et al.*, 1993), protozoa such as *A. castellanii*, *Hartmannella vermiformis* and *Dictyostelium discoideum* were used to study the cellular and molecular pathogenicity of *L. pneumophila* (Rowbotham, 1980b; Hägele *et al.*, 2000). Particularly *D. discoideum* has proven valuable since it can be genetically modified rather easily. The transcriptional responses of *L. pneumophila*-infected macrophages and *D. discoideum* vegetative were analyzed in detail to shed light on the cellular mechanisms of Legionnaires' disease (Farbrother *et al.*, 2006; Losick *et al.*, 2006; Fortier *et al.*, 2011; Steinert, 2011). Moreover, proteomic approaches were shown to be powerful tools to characterize both sides of the host-pathogen interaction (Shevchuk *et al.*, 2009; Urwyler *et al.*, 2009; Hayashi *et al.*, 2010).

Mammalian model animals were established to address immunological, pathological and pharmacological questions of *L. pneumophila* infections, leading to experiments with guinea pigs, mice, rhesus monkeys and marmosets (Baskerville *et al.*, 1981; Fitzgeorge *et al.*, 1983; Blanchard *et al.*, 1987; Jamieson *et al.*, 2013). Wild type mouse strains are, however, resistant to *L. pneumophila* infections, with the exception of a specific inbred strain, which can develop a self-limiting form of legionellosis (Brieland *et al.*, 1994; Wright *et al.*, 2003).

Additionally, invertebrates are increasingly employed to study particular aspects of *L. pneumophila* pathogenicity. These novel model organisms include the nematode *Caenorhabditis elegans*, where the bacterium persists and potentially replicates in the intestinal lumen instead of in phagocytes (Brassinga *et al.*, 2010), the fruit fly

Drosophila melanogaster, which is efficiently killed after abdominal injection with *L. pneumophila* (Kubori *et al.*, 2010), and larvae of the wax moth *Galleria mellonella,* whose phagocytic hemocytes support bacterial replication in LCV-like compartments (Harding *et al.*, 2012).

Despite providing enormous progress in the knowledge about mechanisms of *L. pneumophila* infections, each of the current infection models has intrinsic limitations. Cell culture assays reveal the response of individual cell types, but they lack the complex interaction networks between the highly specialized cell types and extracellular components in the human lung. While many details about the role of intercellular communication in *L. pneumophila* infections are still unknown, this type of signaling was shown to be crucial for the immune response during epithelial infections with *Listeria monocytogenes, Shigella flexneri* and *Salmonella* Typhimurium (Dolowschiak *et al.*, 2010; Kasper *et al.*, 2010). For *S.* Typhimurium, extracellular components are critical since compounds in the intestinal lumen react with reactive oxygen species induced by the infection to provide substrates for the pathogen's energy metabolism (Winter *et al.*, 2010). Similar mechanisms have not been described for *L. pneumophila* yet.

Animal infections require sophisticated intraperitoneal or intratracheal inoculation techniques. Also, given the different genetic and immunologic backgrounds, the adequacy and transferability to humans can be questioned. For example, the transcriptional profile of *Mycobacterium tuberculosis* during infection of mouse lungs strongly differs depending on the mouse strain used, leaving the question which strain is the most suitable model for infections of humans (Talaat *et al.*, 2004). The transferability is particularly dubitable in the case of invertebrate host models, which can only be used to analyze details of infection.

These disadvantages of previous experimental models for infectious diseases in general have led to the development of more sophisticated approaches including tissue samples. Biopsy specimens obtained from patients have long been used to diagnose and describe different infections on the tissue level (Brewer *et al.*, 1976; Winn *et al.*, 1981). The emerging field of tissue microbiology enlarges this approach by experimentally infecting animals to study the course of infections in living tissue (Richter-Dahlfors *et al.*, 2012). Intravital microscopy can be applied to study

infections of exteriorized rat kidneys with uropathogenic *E. coli* (Mansson *et al.*, 2007), but similar experiments with *L. pneumophila*-infected animal lungs have not been described yet. This method enables live *in vivo* monitoring of bacterial adhesion and multiplication, the recruitment of immune cells and blood parameters (Mansson *et al.*, 2007; Melican *et al.*, 2008) and led to the discovery of diversified roles for virulence factors (Melican *et al.*, 2011). However, the interactions of *L. pneumophila* with live host tissue – other than small mammals or invertebrates – are unknown.

3.6 Aim of this work

Besides the inhibitory effect on phagosome-lysosome fusion, the role of OMVs in the interaction between *L. pneumophila* and its hosts has not been described. Mechanistically, the association with host cell surfaces is uncharacterized. It is unknown if OMVs adhere and bind to surface molecules, or if they fuse with the plasma membrane, thereby incorporating OMV components in the host membrane. Thus, this work is to characterize the type of interaction between *L. pneumophila* OMVs and host cell membranes.

Functionally, it is unknown how OMVs, and in particular the degradative enzymes contained in them, contribute to infection on the cellular and tissue level. The presence of these activities suggests a role during the dissemination of infections in infected lung tissue.

Consequently, this work is to investigate the role of OMVs during initial contact with host cell membranes by biophysical methods and during infections on the tissue level in a newly established model comprising living human lung tissue.

4 Materials and methods

4.1 Consumables and chemicals

Consumables like serological pipettes, pipette tips, reaction tubes and multiwell plates were obtained from companies such as Sarstedt, Eppendorf, Greiner bio-one,BD Falcon and Brand. Chemicals were obtained from Sigma Aldrich, Carl Roth, Merck, Invitrogen, Merck and Oxoid if not stated otherwise.

4.2 Cell lines

Cell line	Type	Reference
U937	Monocyte-like cell line from a patient with histiocytic lymphoma,	DSMZ-No. ACC-5, (Sundstrom *et al.*, 1976)
THP-1	Phagocytic cell line from a patient with acute monocytic leukemia	DSMZ-No. ACC-16, (Tsuchiya *et al.*, 1980)

4.3 Bacterial strains

Bacterial strains	Properties	Reference
L. pneumophila Corby	Wild type, Rif^r	(Jepras *et al.*, 1985)
L. pneumophila Corby *dotA*$^-$	Transposon insertion in *dotA,* Km^r	Antje Flieger, RKI Wernigerode
L. pneumophila Philadelphia-1 JR32	Wild type, restriction-deficient, Sm^r	(Marra *et al.*, 1989)

4.4 Bacteriology

4.4.1 Cultivation of *L. pneumophila*

L. pneumophila was cultivated on buffered charcoal yeast extract (BCYE) agar for three days at 37 °C and 5 % CO_2. For liquid cultures, colony material from a BCYE

agar plate was inoculated yeast extract broth (YEB) and incubated at 37 °C on a rotational shaker set to 180-200 rpm.

BCYE agar

5 g	ACES
10 g	Yeast extract
	Add to 900 mL with ultrapure water, adjust pH to 6.9, add to 1 L with ultrapure water
2 g	Activated charcoal
15 g	Agar
	Autoclave and let cool to approx. 50 °C
0.4 g	L-cysteine in 10 mL ultrapure water, sterile-filtered
10 mL	25 g/L $Fe(NO)_3$ x 9 H_2O solution

YEB medium

10 g	ACES
10 g	Yeast extract
	Add to 900 mL with ultrapure water, adjust pH to 6.9, add to 1 L with ultrapure water
0.4 g	L-cysteine in 10 mL ultrapure water
0.25 g	Iron pyrophosphate in 10 mL ultrapure water
	Sterile-filter through 0.22 µm pores into sterile bottles

4.4.2 Cryoconservation of bacterial strains

The bacterial lawn was washed off an agar plate in 1 mL of YEB. To this suspension, 500 µL of 100 % glycerol were added, the resulting mixture was stored at -80 °C. A sterile inoculation loop was used to transfer material from this stock to fresh agar plates when needed.

4.4.3 Enrichment of OMVs

L. pneumophila colony material was transferred from an agar plate into 25 mL of YEB in a 100 mL Erlenmeyer flask as a preculture. After incubation at 37 °C and 200 rpm overnight, 12 mL of this preculture were transferred to a 1 L Erlenmeyer flask containing 420 mL of YEB. This main culture was cultivated at 37 °C and 200 rpm until the culture reached the desired growth phase, usually early stationary growth at an OD_{600} of approximately 2.8-3.2. Bacteria were pelleted for 20 min at 6000 x g; the resulting supernatant was passed through a filter with a pore size of 0.22 µm to hold back residual *L. pneumophila* and debris. The sterile supernatant was ultracentrifuged at 115,000 x g for 3 h. OMVs were pelleted in this step; the supernatant contained soluble proteins (Galka *et al.*, 2008; Jäger *et al.*, 2013c). The OMVs were resuspended in approximately 300 µL 20 mM HEPES, 150 mM NaCl, pH 7.4, and stored at 4 °C. If the OMVs were intended for use in cell culture applications, all steps of the enrichment procedure were carried out under a safety cabinet with sterile reagents. OMVs were quantified in regard to their total protein content with RotiNanoquant based on the Bradford assay (Carl Roth).

4.5 Biophysical methods

All FRET and IR spectroscopy measurements were performed at the Division of Immunobiophysics of the Research Center Borstel under the supervision of PD Dr. Andra Schromm.

Phosphatidylcholine (PC), sphingomyelin, phosphatidylserine (PS) from bovine brain, phosphatidylethanolamine (PE) from *E. coli,* deuterated DMPC (14:0 PC, D54 1,2-dimyristoyl(d54)-*sn*-glycero-3-phosphocholine) and POPS (16:0 D31-18:1 PS, 1-palmitoyl(d31)-2-oleoyl-*sn*-glycero-3-[phospho-L-serine]) were obtained from Avanti Polar Lipids. The dye conjugated-phospholipids *N*-(7-nitro-2,1,3-benzoxadiazol-4-yl)-PE (NBD-PE) and *N*-(rhodamine B sulfonyl)-PE (Rh-PE) for the preparation of phospholipid liposomes were purchased from Molecular Probes/Invitrogen.

4.5.1 Förster resonance energy transfer (FRET) spectroscopy

The incorporation of OMV material into phospholipid liposomes was determined by FRET spectroscopy in a Fluorolog 2 spectrometer (Horiba Scientific; (Schromm *et al.*, 1996; Mashburn-Warren *et al.*, 2008)).

For the preparation of phospholipid liposomes, lipids were dissolved in chloroform. The organic solvent was evaporated under a stream of nitrogen and lipids were resuspended in buffer (20 mM HEPES, 150 mM NaCl, pH 7.4). Liposome formation was induced by sonication for 30 min. To equilibrate liposomes, the preparation was temperature-cycled at least twice between 4 °C und 60 °C, with intense vortexing of the preparations between each cycle, and stored at 4 °C for at least 24 h before using in experiments (Schromm *et al.*, 2007).

The liposomes were labeled with the fluorescent dyes NBD-PE and Rh-PE at a final molar ratio of [PL]:[NBD-PE]:[Rh-PE] = 100:1:1. The emission wavelength of NBD-PE (donor) is in the range of the excitation wavelength of Rh-PE (acceptor), so the two molecules form a FRET pair. This energy transfer between the molecules depends on their spatial distance. FRET was performed as a probe dilution assay, i.e. an incorporation of material into the liposomes increases the liposomal surface and thus the average distance between the labeled phospholipids, leading to a reduction of the FRET efficiency which results in a higher ratio of donor intensity/acceptor intensity ($I_{D[531\ nm]}/ I_{A[593\ nm]}$).

The liposomes used in these experiments were composed of either the neutral phospholipid phosphatidylcholine, negatively charged phosphatidylserine or a mixture of phospholipids mimicking the lipid composition of macrophage membranes (PLMAK), consisting of phosphatidylcholine (PC), phosphatidylserine (PS), phosphatidylethanolamine (PE) and sphingomyelin in a molar ratio of 1:0.4:0.7:0.5; (KRÖNER 1981). Liposomes were diluted to 10 mM in 20 mM HEPES, 150 mM NaCl, pH 7.4, adjusted to a temperature of 37 °C and placed in a glass cuvette with a magnetic stirrer. The emission intensities of the two dyes were adjusted equal at the beginning of each experiment. Fluorescence emission intensities were recorded for 50 s and subsequently, OMVs were added at a final ratio of 1:10 (v/v).

4.5.2 Fourier-transform infrared (IR) spectroscopy

Infrared spectroscopic measurements were carried out with an IFS-55 spectrometer (Bruker) as described previously (Mashburn-Warren *et al.*, 2008). Deuterated 1,2-dimyristoyl-*sn*-glycero-3-phosphocholine (DMPC) or 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phospho-L-serine (POPS) was placed in a CaF_2 cuvette with a 12.5 µm Teflon spacer. Temperature scans were performed automatically between 10 °C and 70 °C with a heating rate of 0.6 °C min^{-1}. Every 3 °C, 200 interferograms were accumulated, apodized, Fourier transformed and converted to absorbance spectra. The main vibrational band used for the evaluation of the gel-to-liquid phase transition of the neutral lipids in the OMV preparations was the symmetrical stretching vibration of the methylene groups v_s (CH_2) located around 2850 cm^{-1} (Brandenburg *et al.*, 1997). The vibrational band of the deuterated lipids was evaluated around 2092 cm^{-1} and could therefore be clearly distinguished from the vibration of the acyl chains of lipids in the OMVs.

4.6 Cell culture

U937 and THP-1 cells were cultivated in RPMI-1640 supplemented with 10 % FCS and 2 mM L-glutamine in 75 cm^2 or 150 cm^2 cell culture flasks at 37 °C and 5 % CO_2. Suspension cell lines were diluted 1:5 to 1:10 in pre-warmed, fresh medium every two to four days depending on when they reached an approximate density of 10^6 cells/mL.

4.6.1 Cryoconservation of mammalian cell lines

To store cells for longer periods of time, 20 mL of a suspension with approximately 10^6 cells/mL was pelleted at 100 x g at 20 °C for 5 min. The pellet was resuspended in 2 mL of freezing medium (RPMI-1640 supplemented with 20 % FCS and 10 % DMSO), transferred to cryotubes and stored in a Nalgene Cryo 1C Freezing Container at -80 °C overnight. The container contained isopropanol and cools down 1 °C per minute. On the next day, the cryotubes were transferred to liquid nitrogen.

To reactivate cryoconserved cells, one tube was rapidly warmed to 37 °C. The suspension was transferred to a tube containing 48 mL of warm cell culture medium. After centrifugation at 100 x g at 20 °C for 5 min, the pellet was resuspended in 15 mL of cell culture medium, transferred to a 75 cm² cell culture flask, and cultivated at 37 °C and 5 % CO_2.

4.6.2 Activation of macrophage-like cells

The number of U937 or THP-1 cells per mL of a culture was determined by counting an aliquot with the help of a Fuchs-Rosenthal chamber. Cells were pelleted from the culture by centrifuging at 100 x g at 20 °C for 5 min. The cells were resuspended in an amount of cell culture medium to yield 10^6 cells/mL. PMA was added to a final concentration of 10^{-8} M to activate and differentiate the cells. 500 µL of the suspension were transferred to each well of a 24-well plate. After 24 h, the cells had adhered to the surface and could be used for further studies.

4.6.3 Assessment of intracellular replication

An overnight culture of *L. pneumophila* was adjusted to 10^7 bacteria/mL in cell culture medium. The monolayer of macrophage-like cells was washed once with warm cell culture medium. Of the inoculum with or without the respective additional components, 500 µL were added to each well. After 2 h at 37 °C and 5 % CO_2, the inoculum was aspirated and the cells were washed once with warm cell culture medium. Extracellular bacteria were killed by adding 500 µL medium containing 100 µg/mL gentamicin to each well for 45 min at 37 °C and 5 % CO_2. Subsequently, the cells were washed twice with cell culture medium and either analyzed for the amount of internalized bacteria or returned to 37 °C and 5 % CO_2 until later time points.

To determine the CFU per well, cells were lysed and detached in 500 µL of cold ultrapure water; wells were rinsed with additional 500 µL of ultrapure water to take up residual cells, resulting in 1 mL of suspension for each well. The suspension was centrifuged at 20,000 x g at room temperature for 5 min to rupture macrophages, and then vortexed for 15 s at full intensity to resuspend the pellet and to destroy residual intact cells. Serial dilutions of this suspension were plated on BCYE agar to determine the amount of bacteria per well. For later time points, the first detachment

step was carried out in the cell culture medium which was already in the wells to include bacteria which had completed one replication cycle and had been released into the supernatant.

4.7 Human lung tissue explants

All experiments involving human lung tissue explants (HLTEs) were carried out at the Department of Clinical and Experimental Pathology of the Research Center Borstel under the supervision of PD Dr. Torsten Goldmann.

Tissue was obtained from patients during pulmonary surgery. To exclude cancerous tissue, samples were taken at least 5 cm from the tumor front. Samples were cut into pieces of approximately 1 cm^3 (0.5 g) with a new scalpel blade to avoid ruptures. HLTEs were stored in RPMI-1640 with GlutaMAX (Gibco) supplemented with 10 % heat-inactivated FCS, 20 mM HEPES and 1 mM sodium pyruvate at room temperature until infection.

4.7.1 Infection of tissue samples

L. pneumophila was cultivated to the early stationary growth phase as described in chapter 4.4.1. The respective *L. pneumophila* strains were adjusted to 10^7 bacteria/mL in RPMI with supplements. Of this inoculum, 2 mL were transferred into cavities of 24-well plates, to which individual HLTEs were added with sterile forceps. The samples were incubated at 37 °C and 5 % CO_2 for up to 48 h. If the samples were to be cultivated for another 24 h, the medium was changed after 48 h. To this end, the tissue sample was transferred to a new well with 1.5 mL of fresh medium with supplements. The 2 mL from the former well were centrifuged at 2000 x g at room temperature for 5 min to pellet extracellular bacteria. The supernatant was discarded; the pellet was resuspended in 500 µL of fresh medium and added to the well with the respective tissue sample.

4.7.2 CFU determination from infected tissue samples

At the indicated time points, individual HLTEs were transferred to tubes with 2 mL of sterile PBS. The tube with PBS was weighed before and after the tissue was added to determine the weight of each tissue sample. Each sample was homogenized with an Ultra-Turrax homogenizer (IKA) for 15 s at full speed. Serial dilutions of the resulting suspension in PBS were plated on BCYE agar to determine the amount of bacteria per g of infected tissue. Between two samples, the dispersing element was sterilized by two washing steps in 70 % ethanol and rinsed once in sterile ddH_2O.

4.7.3 Histological analysis

For histological analysis, a maximum of six identical tissue samples were fixed together in a 50 mL tube containing approximately 30 mL of HOPE solution I (DCS Diagnostics) overnight at 4 °C at the indicated time points after infection. On the next day, the samples were dehydrated in the same tube with 3 mL of acetone at 4 °C for six hours; acetone was changed every 90 min. Subsequently, the dehydrated tissue samples were incubated in liquid paraffin at 54 °C overnight in embedding cassettes, followed by embedding of individual samples in paraffin blocks. These labeled blocks were stored at 4 °C until further analysis.

For microscopic inspection, slides were cut off the paraffin blocks with a microtome and mounted on glass slides. To deparaffinize the samples, slides were incubated in isopropanol at 60 °C for 10 min and subsequently washed in isoporopanol at the same temperature. Slides were air-dried at room temperature and dehydrated in 70 % acetone in DEPC-treated water at 4 °C. To remove acetone, slides were incubated in DEPC-treated water for 10 min and transferred into distilled water at room temperature.

4.7.4 Immunohistochemistry

To visualize *L. pneumophila* or its OMVs in the tissue, mounted and deparaffinized HLTEs were incubated in 3 % H_2O_2 for 10 min to block endogenous peroxidases. The respective primary antibody was diluted in antibody diluent (Zytomed Systems) and applied for 1 h at room temperature. The antibody was linked with post-block

reagent for 10 min. An HRP-conjugated polymer was added for 20 min. The chromogenic reaction was started with permanent AEC (Zytomed Systems) and stopped with distilled water. The slides were counterstained with Mayer's haematoxylin and dehydrated in a graded series of ethanol. Coverslips were mounted with Pertex (Medite).

4.7.5 Transcriptome analysis

RNA was isolated from HOPE-fixed tissue samples as described previously (Marwitz *et al.*, 2011). Quality and integrity of tissue-derived RNA were analyzed with the Agilent RNA 6000 Nano Assay on an Agilent Bioanalyzer. Transcriptome analysis was conducted according to the manufacturer's instructions (Agilent One-Color Microarray-Based Gene analysis, Low Input QuickAmp Labeling Kit, Version 6.6) using 200 ng of total RNA mixed with RNA Spike-In Mix as an in-run quality control (Agilent One Color RNA Spike-In Kit). RNA was converted into double-stranded DNA with MMLV-reverse transcriptase by priming with (d)T-T7 oligonucleotides and subsequent labeling with Cy3 during amplification by T7 RNA polymerase resulting in Cy3-labeled anti-sense cRNA. Labeled cRNA was purified using an RNeasy Mini Kit (Qiagen, Hilden, Germany). Specific fluorescence intensity of labeled samples was calculated with a NanoDrop 2000 spectrophotometer (Thermo Scientific) based on the Cy3 concentration, RNA absorbance ratio and cRNA concentration. 1650 ng Cy3-labeled DNA of each sample was hybridized on one Agilent Human Gene Expression 4x44K microarray. Tiff images of hybridized samples were obtained by scanning with an Agilent SureScan microarray scanner and raw gene expression data were extracted using Agilent Feature Extraction Software (v11.0.1.1) applying the Agilent 1-color Green Gene Expression protocol (v11). Hierarchical clustering, fold change analysis and Gene Ontology term analysis were carried out with Agilent GeneSpring software (v12.1) was used. Quantile-normalized gene expression data were computed from raw data using DirectArray software (Oaklabs, Hennigsdorf, Germany) as described previously (Bolstad *et al.*, 2003).

5 Results

5.1 Interactions between *L. pneumophila* OMVs and the host cell

5.1.1 *L. pneumophila* OMVs during infections of macrophage-like cells

OMVs of other pathogens, including *P. gingivalis*, were shown to influence the course of infection by facilitating adhesion, uptake and intracellular replication (Inagaki *et al.*, 2006). To determine if this is also the case for infections with *L. pneumophila*, OMVs were supplemented to infection experiments with the macrophage-like cell line U937.

A layer of U937 cells was infected with *L. pneumophila* at an MOI of 10. After 2 h, extracellular bacteria were killed with gentamicin and washed away. The amount of intracellular *L. pneumophila* (CFU/mL) was determined by lysing the cells with water and plating the suspension on BCYE agar.

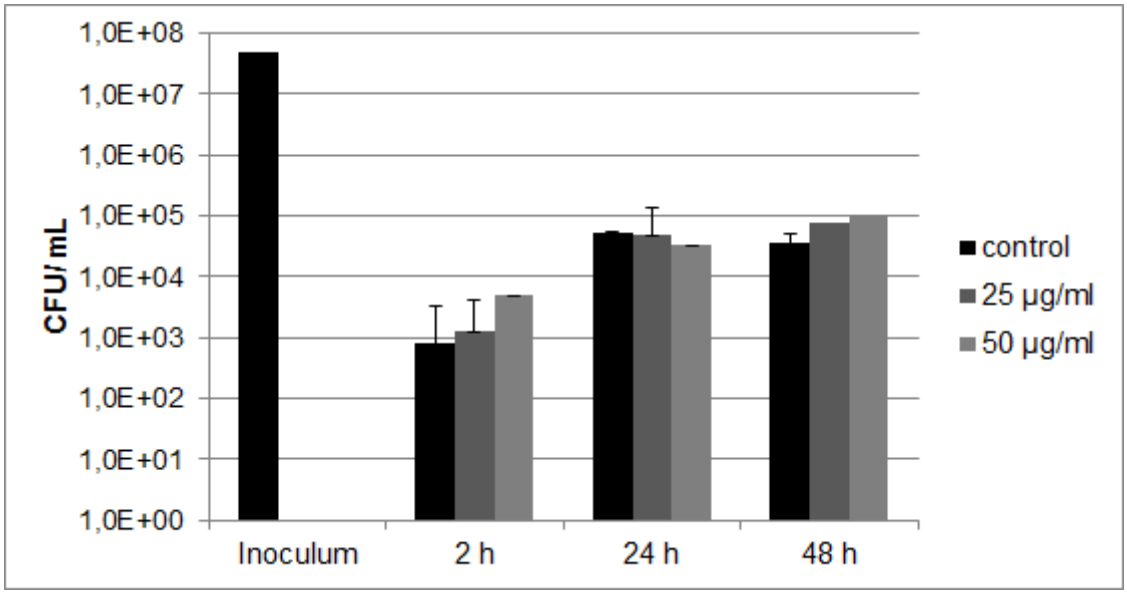

Figure 7: Influence of *L. pneumophila* OMVs on infections of U937 macrophage-like cells; results of a representative triplicate experiment. A monolayer of U937 cells was infected with wild type *L. pneumophila* at an MOI of 10 with additional OMVs at different concentrations (total protein). After 2 h of incubation, non-invaded bacteria were killed with gentamicin and washed away. Cells were lysed with cold ddH_2O; serial dilutions were plated on BCYE agar to determine the CFU/mL at the indicated time points after infection.

The addition of 25 or 50 µg/mL OMVs does not alter the number of *L. pneumophila* which are able to invade the macrophages (Figure 7). In addition, OMVs do not change the number of surviving bacteria inside the macrophages over a course of

48 h significantly. In summary, a quantitative influence of exogenous OMVs on infections of a macrophage-like cell line with *L. pneumophila* is not detectable.

5.1.2 OMVs incorporate into different liposomes

Previously, confocal laser-scanning microscopy images showed that *L. pneumophila* OMVs associate with the plasma membrane of alveolar epithelial cells (Galka *et al.*, 2008). To define the biophysical mechanism of the association of OMVs with host cell membranes, the interaction between OMVs and reconstituted membranes was investigated *in vitro*. To this end, OMVs derived from wild type *L. pneumophila* were incubated with liposomes as a model of the phospholipid bilayer of the cytoplasmic membrane. The phospholipids were labeled with fluorophores forming a FRET pair. If OMV material is incorporated into these liposomes, the average distance between the donor and acceptor molecules increases, resulting in an increase of emission of the donor dye and a weaker fluorescence emission of the acceptor dye, and thus an increased ratio of donor and acceptor signals.

OMVs increased this ratio of donor and acceptor signals in three different liposome preparations composed of phosphatidylserine (PS), phosphatidylcholine (PC) or a mixture of phospholipids which resembles the composition of macrophage plasma membranes (PLMAK), respectively (Figure 8). This effect occurred in two phases. A rapid increase was observed during the first 60 s after addition of OMVs, indicating an incorporation of OMV components into the liposomal membrane. This increase was most pronounced for the negatively charged PS membrane, and weakest for the positively charged PC liposomes. After this initial phase, the ratio slowly and constantly increased during the measurement for all three types of liposomes. While for the PC liposomes saturation was observed after 300 s, PS and PLMAK liposomes did not reach saturation, but showed a further signal increase. In all three liposome preparations, OMVs induced a marked change in FRET compared to the buffer control experiments. Taken together, these data show that *L. pneumophila* OMVs integrate into liposomes with different phospholipid compositions, but most markedly in PS liposomes.

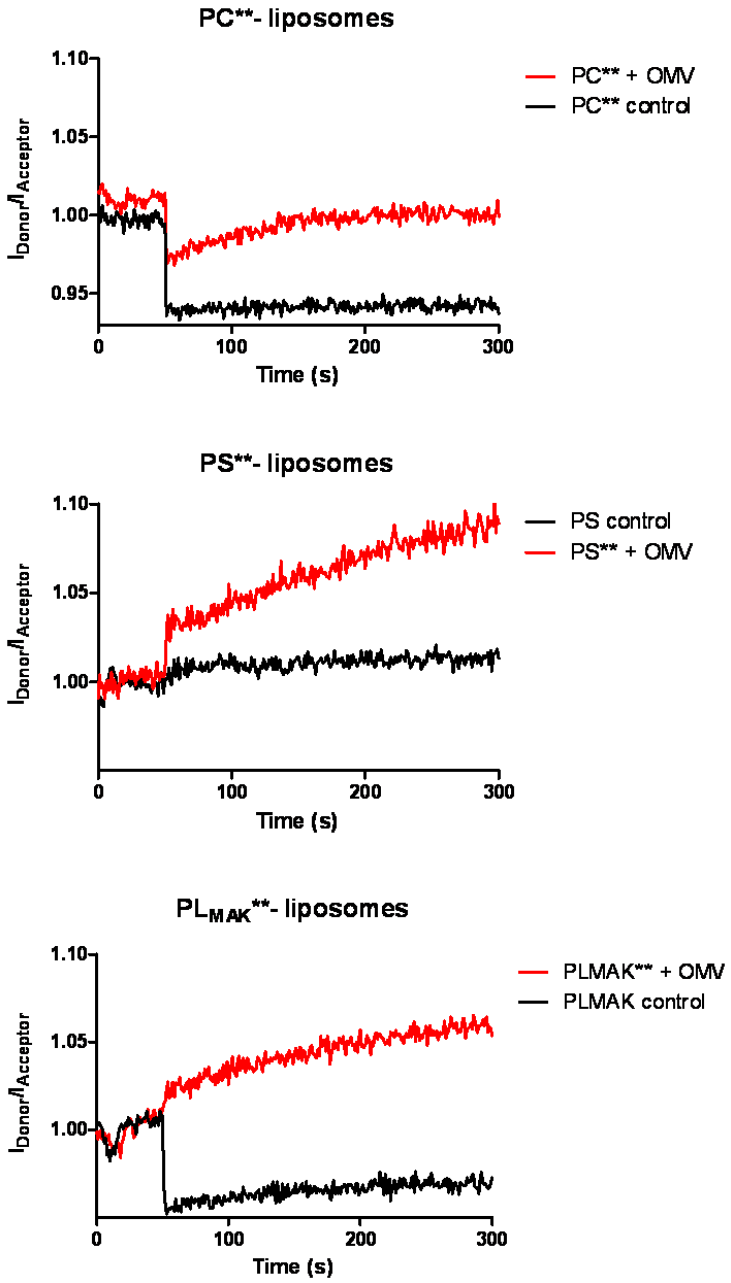

Figure 8: FRET spectroscopy of liposomes composed of fluorescently labeled phosphatidylcholine (PC**), phosphatidylserine (PS**) or a mixture of phospholipids mimicking macrophage membranes (PLMAK**). The ratio of donor and acceptor fluorescence intensities is plotted against time. OMVs were added to the liposome suspension approximately 50 s after the start of the measurement. The control samples contained the respective liposome suspension to which buffer was added. Measurements were performed in duplicates.

5.1.3 OMVs form a mixed phase with eukaryotic membrane lipids

To substantiate and verify the findings from the FRET measurements regarding the fusion of *L. pneumophila* OMVs to phospholipid bilayers *in vitro,* infrared spectroscopy experiments were performed. This method measures the intra-molecular vibration of the fatty acid chains on phospholipid molecules.

With increasing temperature of biological membranes, a transition occurs from a well-ordered gel state to a less ordered liquid crystalline state. This phase transition temperature is a characteristic parameter of each membrane and can be deduced from infrared spectroscopy measurements (Mashburn-Warren *et al.*, 2008). To this end, the temperature of a sample is steadily increased, the infrared absorption by vibration of the acyl chains is determined and the peak position of symmetric stretching vibration of the methylene groups is plotted against the temperature. The inflection point of the resulting graph marks a specific phase transition temperature T_c at which the fluidity of the membranes abruptly increases.

The liposomes in this approach were composed of phospholipids with deuterated fatty acids as their side chains. This modification makes it possible to discriminate whether a signal originates from the fatty acids in OMV membranes or in the deuterated, reconstituted liposomes.

The addition of OMVs induced a strong increase in the phase transition temperature of the deuterated lipids for liposomes composed of PS or PC, respectively (Figure 9). At the same time, the phase transition temperature of the OMV lipids was reduced by several degrees. The mixing of OMVs with liposomes resulted in one main phase transition at a shifted temperature, indicating the creation of a mixed phase composed of non-deuterated lipids from OMVs and deuterated DMPC or POPS molecules, revealing an incorporation of OMV material into target membranes. These findings could be supported in a titration experiment (Figure 9 B). Increasing the volume of OMV solution added to DMPC liposomes demonstrated a dose-dependent shift in the phase transition temperature, again showing one main phase transition. Together, these data strongly support the conclusion that OMVs incorporate in neutral as well as in negatively charged target membranes *in vitro*. This process is most likely attributed to fusion of the OMV membrane with the target membrane.

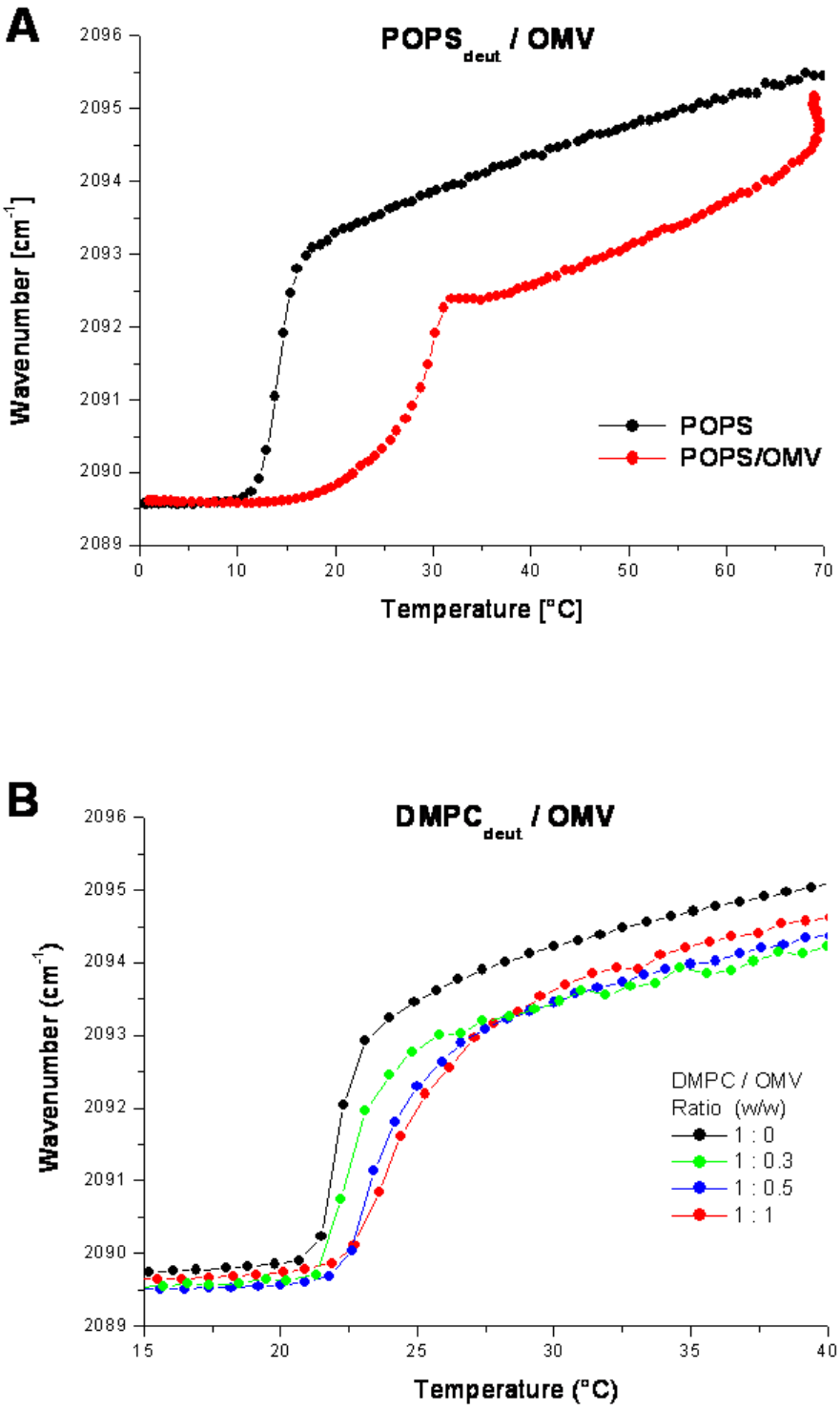

Figure 9: Effect of OMVs on the phase transition temperature of phospholipid liposomes, determined by IR spectroscopy. The absorption of the stretching vibrations of the CH_2 groups in deuterated phospholipid liposomes as a measure of the fluidity was determined in dependence on the temperature. (A) Deuterated POPS in the absence of OMV (black curve) and after addition of OMVs (red curve) to a final weight ratio of 1:1. (B) Deuterated DMPC was mixed with OMV to final weight ratios as indicated.

5.2 Establishment of an infection model with human lung tissue

5.2.1 Replication of *L. pneumophila* strains in human lung tissue explants

Infections with *L. pneumophila* are commonly studied in model systems comprising individual cultured cell types or animal models. Cell culture systems do not include communication between different cell types and extracellular components. The transferability of results from animal experiments to humans is sometimes questionable. To overcome these drawbacks, a novel infection model for *L. pneumophila* was established which consists of living human lung tissue. The samples are taken from the lungs of patients immediately after surgery to ensure vitality *ex vivo* (Figure 10).

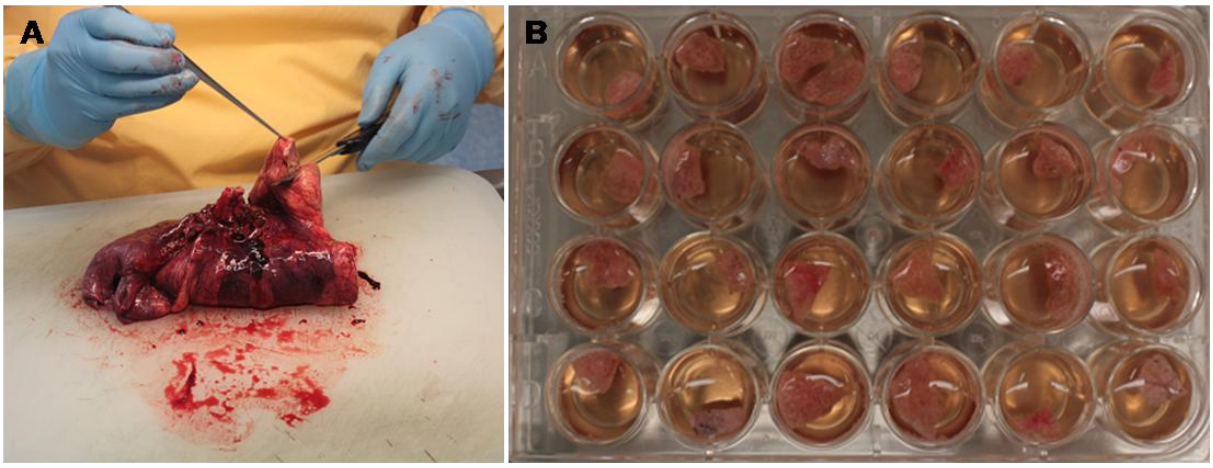

Figure 10: (A) Human lung directly after surgery. The tissue is cut into pieces of approximately 0.5 g and stored in cell culture medium until further experiments. (B) Individual lung tissue explants, abbreviated HLTEs, are cultivated in 24-well plates, where they can also be co-incubated with *L. pneumophila* or its OMVs.

To be suitable as a model for infections with *L. pneumophila*, HLTEs have to support the intracellular replication of the pathogen. To assess this question, tissue samples were infected with 2 x 10^7 *L. pneumophila*. The bacterial load per gram of tissue was determined 2, 24, 48 and 72 h after infection by weighing and homogenizing the samples and subsequent plating of the suspension on BCYE agar.

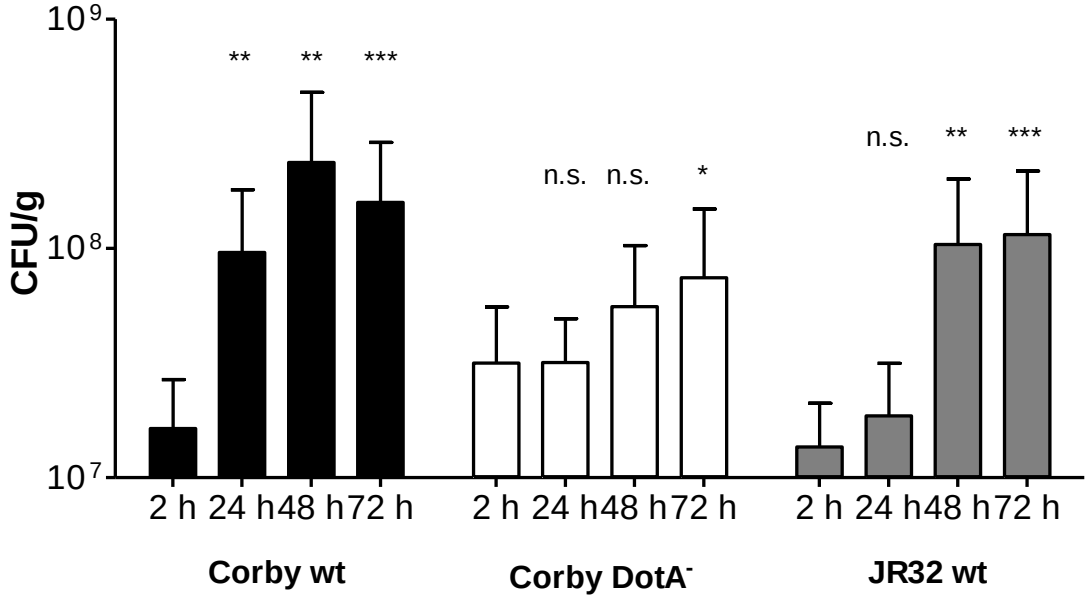

Figure 11: Replication of *L. pneumophila* Corby (wild type; wt), the isogenic DotA-deficient strain and *L. pneumophila* Philadelphia-1 JR32 (wt) in HLTEs; modified from (Jäger *et al.*, 2013b). Infected HTLEs were weighed, homogenized and plated on BCYE agar at the indicated timepoints after infection. The graph visualizes means and standard deviations of triplicate experiments with tissue from eight donors. The statistical significance of the means was compared to the respective CFU/g at 2 h after infection. *: $p \leq 0.05$; **: $p < 0.01$; ***: $p < 0.001$; n.s.: not significant ($p > 0.05$) as determined by the student's *t*-test for samples with identical variance.

The number of wild type *L. pneumophila* Corby increases by approximately 10-fold in the first 24 hours of infection (Figure 11). Until 48 h after infection, the increase continues at a lower rate. After 48 h, the amount of bacteria decreases slightly. For an isogenic DotA-deficient strain, which is incapable of type IVB secretion, a significant bacterial replication cannot be observed over the course of 48 h; the only significant increase in the amount of bacteria can be detected 72 h after infection. The replication of the wild type strain *L. pneumophila* Philadelphia-1 JR32 commences only after 24 h of infection and does not significantly increase between 48 and 72 h. Neither of the strains used in these experiments replicates markedly after the first 48 h of infection. For all subsequent experiments, *L. pneumophila* Corby, its outer membrane vesicles and isogenic mutants were used.

5.2.2 Localization of *L. pneumophila* and its OMVs in human lung tissue explants

Clinical reports about patients with Legionnaires' disease describe the pathogen to be localized predominantly in alveolar phagocytes (Winn *et al.*, 1981). Under laboratory conditions, *L. pneumophila* can also invade and exploit alveolar epithelial cells for replication (Mody *et al.*, 1993). Besides the previously reported association of outer membrane vesicles with the surface of alveolar epithelial cells (Galka *et al.*, 2008), it is unknown if and how OMVs contribute to the pathogenesis of Legionnaires' disease on the tissue level.

In infected HLTEs, the localization of *L. pneumophila* is determined via immunostaining with antibodies against the surface proteins Mip and MOMP within 48 h after infection. The strongest signals come from the surface and the interior of alveolar macrophages, confirming them as the predominant host cell type (Figure 12 C, D). At sufficient magnification, groups of *L. pneumophila* can be detected in *Legionella*-containing vacuoles in alveolar macrophages (Figure 13). In addition, many bacteria can be found adhering to the connective tissue and the alveolar surface, particularly close to sites of tissue destructions (Figure 12 D). In some cases, *L. pneumophila* can be detected in alveolar epithelial cells, thus confirming previous findings from *in vitro* studies (Figure 14).

L. pneumophila OMVs are detected on the surface and also in the cytoplasm of alveolar macrophages by immunostaining with an anti-MOMP antibody (Figure 12 F). Mip is detected to a lower extent in OMV-treated tissue samples.

The staining intensity of the anti-Mip antibody tends to be generally weaker than that of the anti-MOMP antibody. Uninfected tissue samples do not yield positive signals for either of the antibodies (Figure 12 A, B).

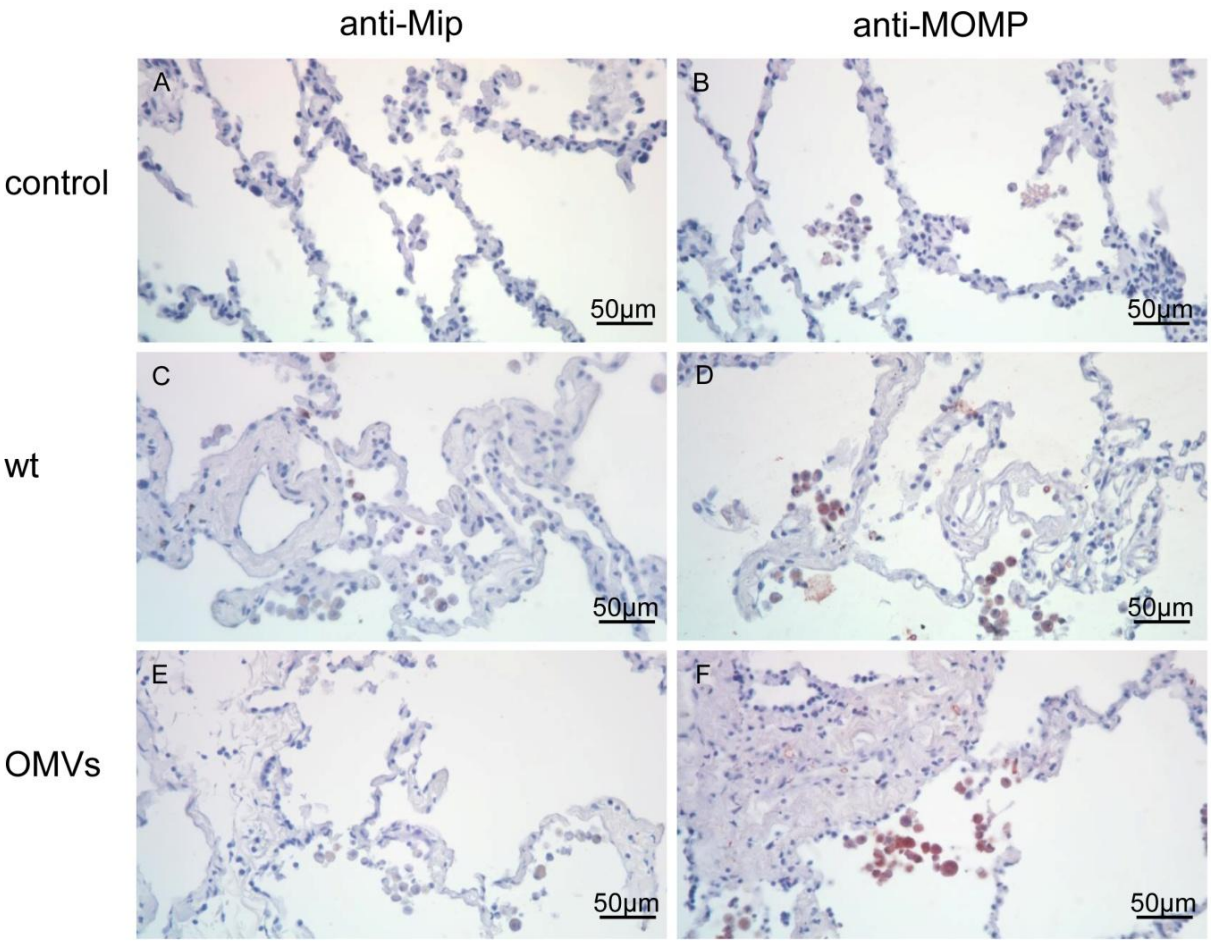

Figure 12: Detection of *L. pneumophila* and OMVs in the alveolar compartment; from (Jäger *et al.*, 2013b). All images at 40 x magnification and all HLTEs stained with haematoxylin after 24 h of incubation. Immunohistochemistry with anti-Mip **(A, C, E)** and anti-MOMP antibodies **(B, D, F)** followed by visualization with HRP polymer and permanent AEC (red signals). Uninfected controls remain negative for both antibodies (A, B); *L. pneumophila* (wt) is mainly observed in alveolar macrophages with both antibodies (C, D). In contrast to the detection of the whole pathogen, OMVs were only detected sufficiently with the anti-MOMP antibody (F).

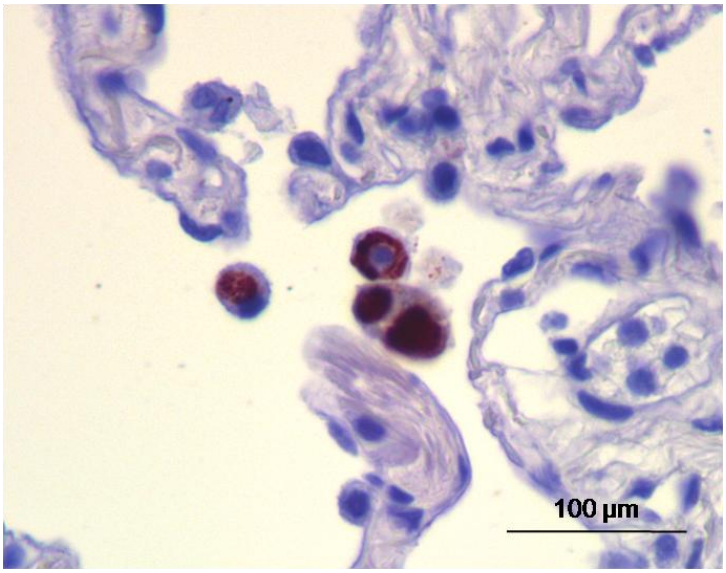

Figure 13: Immunostaining visualizes groups of *L. pneumophila* cells in LCVs within alveolar macrophages. Immunohistochemistry of a haematoxylin-stained HLTE with an anti-Mip antibody 24 h after infection at 400 x magnification.

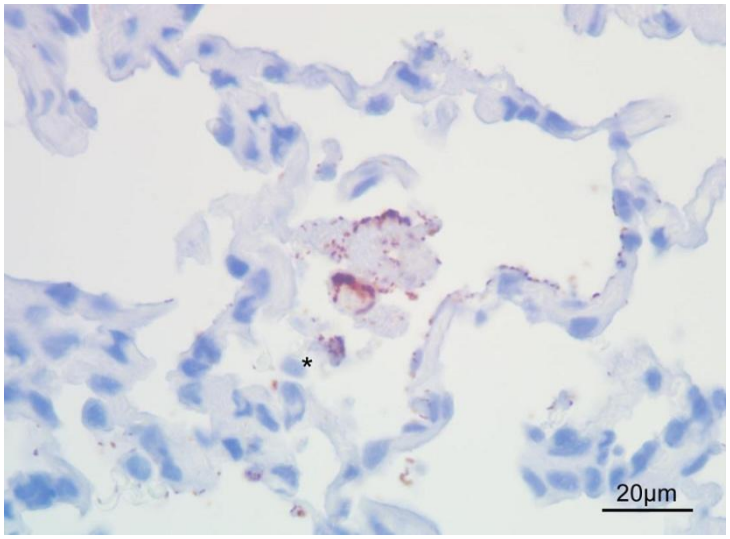

Figure 14: *L. pneumophila* adheres extracellularly to the alveolar compartment and infects epithelial cells (asterisk). Immunostaining anti-Mip of a haematoxylin-stained HLTE 24 h after infection at 100 x magnification.

5.2.3 Tissue damage after infection and OMV stimulation

A scoring was set up to quantify the damage to tissue architecture in HLTEs after infection with *L. pneumophila* or incubation with OMVs. This scoring was applied to HOPE-fixed, haematoxylin-eosin-stained sections of the respective samples at 2, 24 and 48 h after infection. Three damage phenotypes occurred most dominantly and contributed to the overall damage score of the samples: disintegrated connective

tissue in alveolar septa, detaching alveolar epithelia and protein exudate in the alveoli (Table 1, Figure 15).

Table 1: Damage score categories of HLTEs shown as median ± interquartile range; from (Jäger *et al.*, 2013b). The severity of each phenotype was judged on a scale from 0 (does not occur) to three (severe damage as the dominating pattern) for sections from 6-9 donors. The total damage score was calculated by adding up the specific damage scores of each donor at a given time point.

		Protein exudate	Epithelial delamination	Septal damage	**Total damage score**
2 h	Control	0 ± 1	0 ± 0	0 ± 0	**1 ± 1**
	wt	1 ± 2	0 ± 1	0 ± 0	**2 ± 2**
	DotA$^-$	1.5 ± 2.75	0 ± 0	0 ± 0	**1.5 ± 1.75**
	OMVs	0 ± 1	0 ± 0.5	0 ± 0.5	**0 ± 2.5**
24 h	Control	1 ± 2	1 ± 1	0 ± 1	**2 ± 2**
	wt	2 ± 2	1 ± 1.25	2 ± 1	**5 ± 1.5**
	DotA$^-$	1 ± 1	1 ± 0	1 ± 0	**2.5 ± 1.5**
	OMVs	1 ± 1.5	2 ± 1	2 ± 1.5	**6 ± 2**
48 h	Control	0.5 ± 1.25	0.5 ± 1	1 ± 0	**3 ± 1.25**
	wt	2 ± 1	2 ± 1	3 ± 2	**6 ± 1**
	DotA$^-$	1 ± 0.75	1 ± 0	1.5 ± 1	**4 ± 0.75**
	OMVs	1 ± 1	2.5 ± 2	2.5 ± 2	**5.5 ± 1.75**

All three types of damage can be observed more frequently and appear stronger with increasing incubation times (Table 1). Intraalveolar protein exudate can be detected to some extent already 2 h after infection. The delamination of epithelia and the disintegration of septa appear to commence 24 h after infection. All three tissue integrity criteria reach their maximum at 48 h after infection, which is also reflected in the overall damage score (Figure 16 A).

At 24 and 48 h after infection, the overall damage score of wild type-infected HLTEs is significantly higher than that of uninfected samples (Figure 16 A). Interestingly, the tissue damage caused by incubation with OMVs is comparably high. Infecting HLTEs with a DotA-deficient mutant strain results in a damage score which does not differ significantly from uninfected controls.

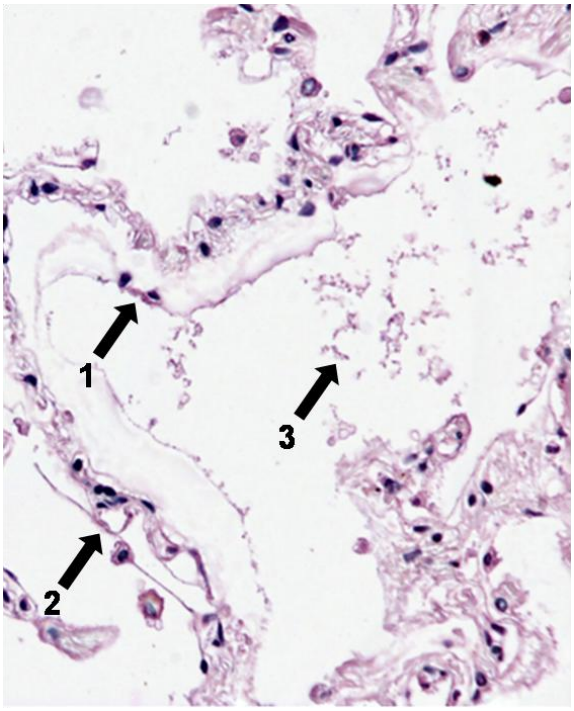

Figure 15: Overview of the observed tissue damage phenotypes after infection of human lung tissue with *L. pneumophila*. Haematoxylin-eosin-stained section of an HLTE after 24 h of infection with wild type *L. pneumophila* at 400 x magnification. (1) Epithelial cells delaminate from the connective tissue, (2) an interalveolar septum disintegrates, (3) protein aggregate can be detected in the alveolar lumen.

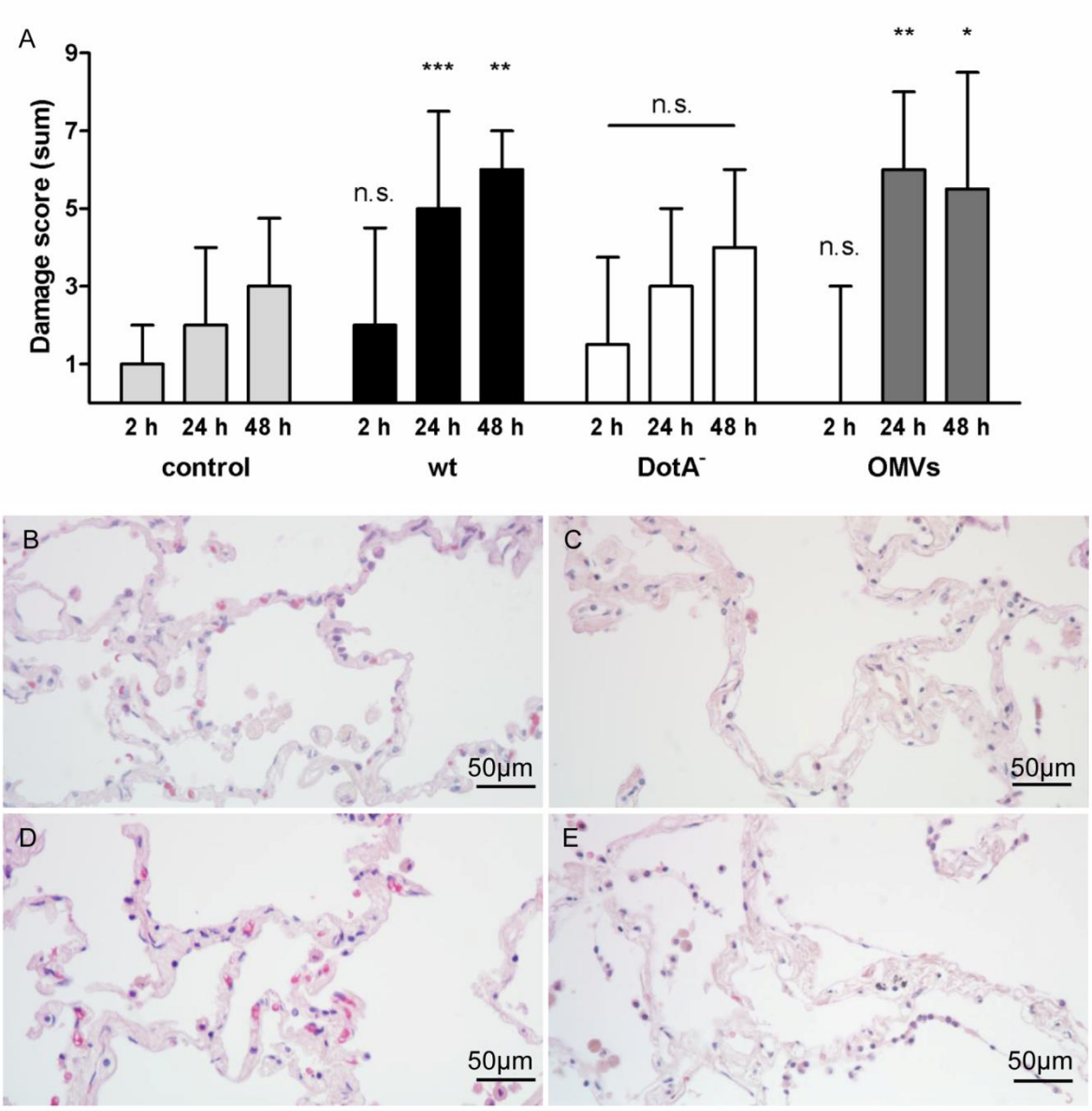

Figure 16: Tissue damage in HLTEs; from (Jäger *et al.*, 2013b). A) For each time point and condition, tissue damage was classified in samples from 6-9 donors in the three categories protein exudate, delamination of epithelial cells and integrity of alveolar septa on a scale from 0-3 and added up. Total damage score medians and interquartile ranges were calculated; values of infected or OMV-stimulated samples were compared to the uninfected control at the respective time point with the Mann-Whitney test with a Bonferroni-corrected confidence interval of 98.3 %. *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$. **(B)** Uninfected control, **(C)** *L. pneumophila* wildtype-infected HLTE, **(D)** sample infected with the DotA-deficient mutant, **(E)** sample incubated with 100 µg/ml OMVs; haematoxylin-eosin-stained sections of HLTEs after 24 h of incubation. Infection with *L. pneumophila* wildtype leads to loosening of collagen backbones in alveolar septa and delamination of epithelial cells (C). The DotA-deficient mutant does not show a significant difference compared to the uninfected control (D). Incubation with OMVs resulted in severe tissue damage, including a wide-spread delamination of epithelial cells and loss of septal integrity (E).

5.2.4 Transcriptional response of infected HLTEs

To characterize the tissue response to infection with *L. pneumophila* Corby, RNA was isolated from HLTEs. Transcriptome data were obtained from samples from two patients in a preliminary analysis. Overall, 2499 genes were found to be differentially regulated with a fold change ≥ 2.0 24 h after infection with *L. pneumophila* (Table A1 in the appendix). Eight Gene Ontology terms are significantly enriched among the regulated genes (

Table 2). Distinct response levels could be observed (Figure 17 A).

Table 2: Gene Ontology term analysis of genes differentially regulated after infection of HLTEs with *L. pneumophila;* from (Jäger *et al.*, 2013b). 2499 genes with a fold change ≥ 2 were used as input for a Gene Ontology analysis. A Benjamini-Yekutieli correction was applied and a p-value ≤ 0.05 was set as the cut-off.

GO accession	**GO term**	**Corrected p-value**
GO:0005576	extracellular region	0.00003
GO:0044421	extracellular region part	0.00003
GO:0005615	extracellular space	0.00020
GO:0002376	immune system process	0.00854
GO:0005929	cilium	0.01026
GO:0042953	lipoprotein transport	0.01302
GO:0035085	cilium axoneme	0.02505
GO:0005930	axoneme	0.03395

Uteroglobin was identified as one of the genes upregulated after infection (2.18 log2-fold, Table 3). Targeting uteroglobin on the protein level via immunostaining did not reveal a marked difference between infected and uninfected samples. Alveolar macrophages were predominantly positive for uteroglobin (Figure 17 B, C).

Among the downregulated genes, MARCO, the macrophage receptor with collagenous structure, was detected (Table 3). MARCO is strongly expressed in uninfected tissue, and is 1.96 log2-fold downregulated after infection with *L. pneumophila* (Figure 17 D, E). Immunostaining verified this finding, revealing a strong MARCO signal on alveolar macrophages in non-infected HLTEs (Figure 17 D) and a reduced expression on macrophages at sites of tissue destruction after infection (Figure 17 E).

Table 3: Differential gene expression of uteroglobin and MARCO after infection with wild type *L. pneumophila;* from (Jäger *et al.*, 2013b). Quantile-normalized expression levels of uteroglobin and MARCO in two donors obtained from microarray raw data using Direct Array software.

			Relative expression level		Log2 fold change
Gene ID	Name	Donor	Control	Wildtype	
NM_003357	Uteroglobin	1	7288.43	28741.66	
		2	1157.49	6897.58	
		mean	4222.96	17819.62	**+ 2.18**
NM_006770	MARCO	1	3190.08	958.49	
		2	9088.06	2412.81	
		mean	6139.07	1685.65	**- 1.96**

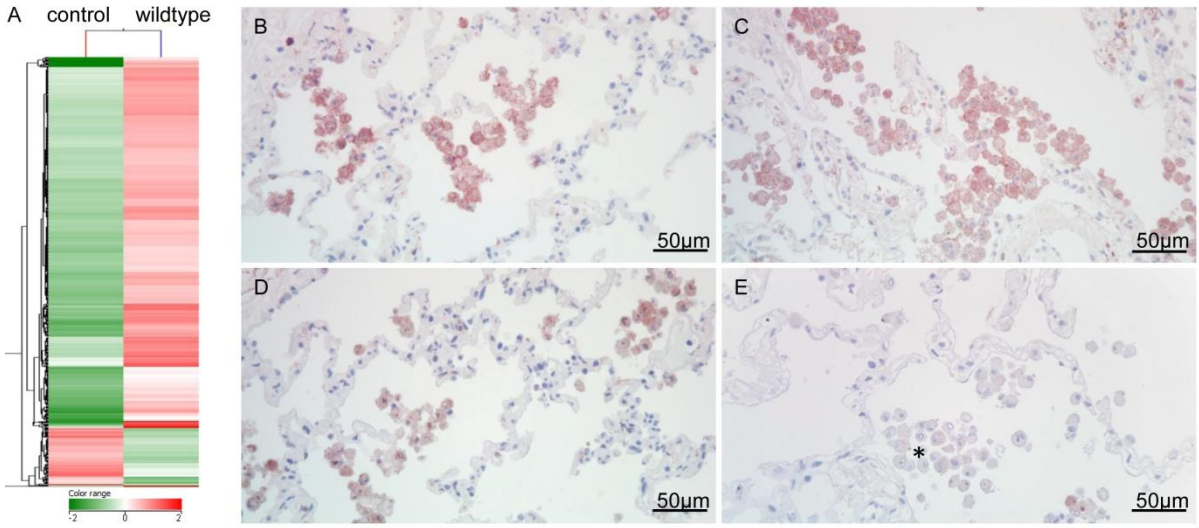

Figure 17: Transcriptional response of *L. pneumophila*-infected HLTEs and targeting of candidate genes on the protein level; from (Jäger *et al.*, 2013b). **(A)** Heat map analysis and hierarchical clustering of 2499 genes with a log2-fold change ≥ 2. RNA was isolated from *L. pneumophila* wildtype-infected and uninfected HLTEs after 24 h of incubation (n = 2 each) to analyze the acute phase of infection. Distinct clusters were found to be differentially regulated after infection. **(B, C)** Immunohistochemistry against uteroglobin and MARCO **(D, E)** on HLTEs after 24 h of incubation with medium (B, D) and *L. pneumophila* (C, E). Both proteins were mainly detected on alveolar macrophages. MARCO was observed to be downregulated over the course of stimulation at sites of tissue damage (* in E). Images of haematoxylin-stained HLTEs were taken at 40x magnification with permanent AEC (red signals) as the chromogen.

6 Discussion

Legionnaires' disease is an atypical form of pneumonia caused by the bacterium *L. pneumophila*. Like many other Gram-negative bacteria, *L. pneumophila* sheds vesicles from its outer membrane which are enriched in virulence-related proteins (Galka *et al.*, 2008). They are therefore suggested to be involved in host-pathogen interactions. In this study, biophysical measurements determined the mode of interaction between *L. pneumophila* OMVs and model host membranes to include incorporation of OMV material into membranes *in vitro.* In contrast, the supplementation of macrophage infection experiments with additional OMVs does not alter the course of infections with *L. pneumophila*, indicating a role for OMVs in pathogenesis that exceeds the cellular level, e.g. involving the extracellular matrix or the architecture of the infected tissue.

To study the effects of *L. pneumophila* and its OMVs on the tissue level, a novel infection model comprising living human lung tissue samples was established. These samples enable the pathogen to replicate within alveolar macrophages and alveolar epithelial cells and to damage tissue architecture in close accordance with previous descriptions of specimens from Legionnaires' disease patients. After the thorough validation of the infection model by microbiological and histological methods, *L. pneumophila* OMVs were found to contribute to the characteristic histopathologic features of Legionnaires' disease considerably. Moreover, the novel model can be used to analyze further open questions in regard to *L. pneumophila* virulence on the tissue level.

6.1 Interactions between *L. pneumophila* OMVs and the host cell

6.1.1 Incorporation of *L. pneumophila* OMVs into target membranes

Previous studies showed that OMVs shed by *L. pneumophila* associate with the surface of alveolar epithelial cells (Galka *et al.*, 2008). It was unclear if they merely adhere to surface molecules or if OMVs actually induce fusion, thereby incorporating OMV material into the plasma membrane. To distinguish between adhesion and incorporation, the association between *L. pneumophila* OMVs and reconstituted

membrane systems was characterized *in vitro*. Two different approaches were taken to address this question.

FRET spectroscopy measurements showed that OMV material is incorporated into phospholipid liposomes. Thereby, the liposome surface is increased, resulting in less energy transfer between the fluorophores. The process commences with a rapid initial phase with a strong increase in the ratio of I_D/I_A and can most likely be attributed to fusion of the OMVs and the liposomal membranes. This step is followed by a second phase of a slower but steady increase of the signal ratio, indicating that the process has not yet reached saturation at the end of the measurement.

OMVs were integrated into different liposomes composed of phosphatidylserine (PS), phosphatidylcholine (PC) and a mixture mirroring the lipid composition of macrophages (PLMAK), respectively. The FRET signal from measurements with PS liposomes is the strongest while that of the PC liposomes is less pronounced. This shows that the incorporation partially depends on the liposomal surface charges. PC is a zwitterion with a positively charged head group, PS is negatively charged with a neutral head group and the net charge of PLMAK liposomes is slightly negative.

The integration of OMV lipids into target membranes was confirmed by infrared spectroscopy. In these experiments, OMV lipids and phosphatidylcholine or phosphatidylserine form a mixed lipid phase with a phase transition temperature different than those of the two initial components. The phase transition temperature of the target membrane is increased by the incorporation of OMVs, resulting in a more rigid membrane after the incorporation of OMV components.

It is interesting to speculate that fusion of OMVs from *L. pneumophila* or another pathogen with host membranes can locally influence physical membrane properties. As a consequence, phagocytosis might be modified and signaling processes may be affected, as these two mechanisms are influenced by membrane fluidity (Helmreich, 2003). The recruitment, localization and function of membrane proteins in all subcellular compartments also depends on properties of the respective membrane (Lundbaek *et al.*, 1994; Delmas *et al.*, 2011; Maccarrone *et al.*, 2011; Finka *et al.*, 2013) and could be affected by incorporated OMV material. Whether the fluidity of host cell membranes changes after fusion with *L. pneumophila* OMVs will be an interesting aspect of future studies. OMVs integrated into host membranes are,

however, most likely to affect specific localized domains rather than the overall fluidity of the cytoplasmic membrane.

In addition, phosphatidylethanolamine molecules from OMVs may contribute to the alteration of biophysical properties of target membranes. In preliminary phospholipid analyses, *L. pneumophila* OMVs were shown to contain high percentages of PE. This neutral phospholipid is thought to dilute the negative charge of PS-rich membranes, thereby locally compensating the membrane charge and influencing the subcellular localization of proteins (Yeung *et al.*, 2009). This process could also contribute to the differential localization of membrane proteins which are normally recruited by PS. Some of the host proteins detectable on the LCV may in fact be recruited in this manner.

The stronger interaction of OMVs with PS membranes is particularly interesting. LPS molecules, including those on OMVs, carry a negative charge due to phosphate groups in their lipid A moiety. Spontaneous interactions between two negatively charged lipids, i.e. LPS in OMVs and PS in liposomes, are unfavorable. However, the charge can be compensated by other factors, as it is the case for *Salmonella enterica* LPS, which integrates into PS liposomes only after binding to a host protein (Schromm *et al.*, 1996). Since the *in vitro* fusion of *L. pneumophila* OMVs with membranes in this study does not require exogenous lipid transport proteins, the assays can be considered a suitable model system to study membrane fusion in general. It is unknown which OMV-associated molecule mediates the fusion processes between the respective OMV and its target membrane. Possible candidates include the lipid-modifying enzymes lpg0502 (phosphatidylcholine-hydrolyzing phospholipase), lpg1353 (acetyl-CoA acetyltransferase), lpg1455 (phospholipase C) and lpg2837 (lysophospholipase A) which were detected in *L. pneumophila* OMVs (Galka *et al.*, 2008).

Alternatively, some lipid molecules tend to destabilize membranes, thereby facilitating fusion processes with other membranes. This is the case for lysophospholipids (Haydon *et al.*, 1963; Lucy, 1970). In fact, small amounts of lysophosphatidylethanolamine were detected in OMVs in preliminary analyses. To test the hypothesis that lysophospholipids contribute to the fusion process between OMVs and target membranes, tocopherol could be used to inhibit membrane destabilization by lysophospholipids in future studies (Kagan, 1989).

6.1.2 Potential subcellular targets of *L. pneumophila* OMVs

It is tempting to postulate fusions of OMVs and other membranes than the plasma membrane, particularly because of the preferential integration of *L. pneumophila* OMVs into PS membranes. PS is a common constituent of the inner, but not the outer leaflet of the plasma membrane of eukaryotes. Interestingly, significant amounts of PS can also be detected at the luminal leaflet of the ER (Fairn *et al.*, 2011). ER vesicles fuse with the *Legionella*-containing vacuole shortly after uptake of the pathogen (Robinson *et al.*, 2006). Thereby, they may transfer PS to face *L. pneumophila* in host cells. While the PS content of the LCV membrane was shown to be low at 4-6 h after infection, it is possible that LCVs do contain PS shortly after uptake of the pathogen (Yeung *et al.*, 2009). It is conceivable that OMVs shed from the *L. pneumophila* surface fuse with the LCV membrane at early infection stages, where they might contribute to the tremendous changes in LCV composition (see chapter 3.2.2).

The fusion between OMVs and the LCV membrane may also result in the disruption of the LCV membrane in later stages of infection, when the PS content of the LCV is unknown. The disruption of the LCV would release the pathogen into the cytosol. Electron micrographs show that in infected human macrophages and amoebae, *L. pneumophila* escapes from the LCV and can be detected in the cytoplasm in large numbers 18-24 h after infection (Molmeret *et al.*, 2004). In the same time frame, large numbers of OMVs were found in LCVs in *D. discoideum* (Galka *et al.*, 2008). Thus, destructive enzymes from OMVs could disrupt the LCV membrane and enable the pathogen to escape into the cytosol. Interestingly, the *L. pneumophila* type II secretion system, which exports these enzymes, is not required for LCV disruption, indicating that another export mechanism mediates this process (Molmeret *et al.*, 2004). It is conceivable that the aforementioned hydrolyzing enzymes, including phospholipases and proteases, are exported in OMVs; and in fact several of them were detected in *L. pneumophila* OMVs (Galka *et al.*, 2008). The fusion of enzyme-packed OMVs would release the degradative activities in close proximity to their potential substrates in the LCV membrane. Studies with mutants defective in these enzymes could show if they are involved in the proposed egress of *L. pneumophila* into the cytosol. Furthermore, OMVs could contribute to the disruption of the PS-rich

plasma membrane when the host cell is lysed, resulting in the release of the bacteria into the surrounding medium.

Since host cell lipid rafts are often sites of attachment for pathogens, the interaction of OMVs with cholesterol-rich domains in model membranes and host cell membranes is of interest. For the fusion of *P. aeruginosa* OMVs with host cells, a functional actin cytoskeleton and lipid rafts were suggested be required (Bomberger *et al.*, 2009). The involvement of these two structures can be excluded for integration of *L. pneumophila* OMVs into eukaryotic model membranes, since the biophysical experiments in this study were performed with homogenous liposomes *in vitro,* where lipid rafts and the host cytoskeleton were not present.

In the same study on vesicles from *P. aeruginosa*, proteins from the OMV lumen were shown to be delivered into the host cell cytoplasm (Bomberger *et al.*, 2009). Future analyses can address the translocation of *L. pneumophila* proteins into host cells via this unusual mechanism, preferably by easily detectable OMV proteins. For instance, the genomically encoded β-lactamase of *L. pneumophila* is usually located in the periplasm and is thought to be contained in OMVs, as well. This enzyme activity can be exploited to study if it is translocated into the host cell cytosol after fusion of OMVs with the plasma membrane by a commercially available fluorescence-based assay (Zlokarnik *et al.*, 1998).

6.1.3 OMVs during infection of macrophages

The effects of fusion events between *L. pneumophila* OMVs and host cells, particularly macrophages, are unclear. For other human pathogenic bacteria, it was demonstrated that OMVs enhance the adhesion of bacteria to the host cell surface (Inagaki *et al.*, 2006). To determine whether this is also holds true for *L. pneumophila* infections, human macrophage-like cells were infected with the pathogen supplemented with additional OMVs from the same strain.

Intriguingly, additional *L. pneumophila* OMVs do not influence the quantitative outcome of an infection with this pathogen within 48 hours. They do not facilitate bacterial uptake, e.g. by triggering phagocytosis, since the amount of invaded *L. pneumophila* after 2 h is similar to that in control experiments. Furthermore, the

intracellular replication rate is unchanged, revealing that additional exogenous OMVs do not contribute to the establishment of the intracellular niche. It can be ruled out that *L. pneumophila* utilizes OMV components as nutrients within host cells.

It is unlikely that higher amounts of OMVs will lead to different results. The OMV concentrations applied in these experiments are already rather high. The average yield is approximately 1 mg of OMVs (total protein content) from 400 mL of liquid culture. Thus, one cavity of an infection assay supplemented with 50 µg/mL OMVs contains already as much OMV material as is produced by 10 mL of a *L. pneumophila* culture in 18 hours. Thus, this amount is already higher than that it could occur during an infection *in vivo*.

These findings do not necessarily implicate that OMVs are not involved in the propagation of macrophage infections at all. It is likely that the endogenous amount of OMVs is sufficient to permit a maximally successful invasion and replication, and that additional exogenous OMVs do not improve the infection outcome for the pathogen.

While OMVs of other species were shown to have diverse effects on other bacteria, none of these could be reported for *L. pneumophila* OMVs (Krüger, 2011). Bactericidal activity and integration of OMV components into several target bacteria could not be observed so far. The ecological role of *L. pneumophila* OMVs remains unclear; adverse effects on predatory amoebae and competing microorganisms are conceivable.

6.2 An *ex vivo* model for the analysis of early events in the pathogenesis of Legionnaires‘ disease

6.2.1 Establishment of an infection model for *L. pneumophila* comprising living human lung tissue

Some events in the establishment of Legionnaires’ disease cannot be studied using cell culture systems. Examples of these events include effects of the infection on the tissue level, e.g. the destruction of supracellular structures or the influence of the pathogen on communication between different host cell types. Model animals such

as guinea pigs can help overcome these drawbacks, but if and how the findings from animal experiments can be transferred to the actual disease in humans is disputable.

Explanted human tissue is a model system which combines the advantages of human cells and complex interactions between different cell types. It allows for the analysis of interactions between a pulmonary pathogen and the very structures where pathogenesis occurs. Infections with *Chlamydophila pneumoniae, Streptococcus pneumoniae* and *Haemophilus influenzae* were studied in explanted human lung tissue in regard to particular aspects (Rupp *et al.*, 2004; Xu *et al.*, 2008; Drömann *et al.*, 2010). Caveats of using human tissue samples include donor diversity and clinical parameters of the patients. High-dose antibiosis might impact bacterial viability in the tissue, while other drugs may influence the response to infection. Higher sample sizes and consideration of medical records help reduce these drawbacks.

To make sure that human lung tissue explants are a valid model for infections with *L. pneumophila*, they are to support the replication and correct localization of the pathogen; and the tissue damage resulting from the infection has to be similar to descriptions from patient material. The evaluation of the experiments in this study proves that the wild type *L. pneumophila* strains Corby and Philadelphia-1 JR32 replicate successfully and significantly in explanted human lung tissue samples within 72 h hours of infection. A DotA-deficient strain fails to multiply in the first 48 h. Since this strain does not show any replication defects in liquid media, this finding demonstrates that the wild type strains indeed proliferate intracellularly, which the mutant strain fails to accomplish. Importantly, the replication rate of the wild type in tissue samples is quantitatively comparable to that in cell culture-based assays (Juli *et al.*, 2011). No data are available about the replication rate of *L. pneumophila* in infected patients. Thus, this study gives first information about this crucial event in the pathogenesis of Legionnaires' disease.

The wild type strain *L. pneumophila* Philadelphia-1 JR32 does not replicate in HLTEs as successfully as *L. pneumophila* Corby. This confirms a previous finding describing Corby as an extremely virulent strain in a guinea pig model of Legionnaires' disease (Jepras *et al.*, 1985). JR32 on the other hand already showed a decreased adherence to human host cells and a less efficient prevention of phagosome-lysosome fusion compared to other wild type strains (Samrakandi *et al.*, 2002). Since

the integrity of HLTEs cannot be maintained for longer than 72 h, JR32 was excluded from subsequent experiments and Corby was chosen as the reference wild type.

It is unknown if outbreaks of Legionnaires' disease differ in intensities or incubation time depending on the responsible *Legionella* strain, but it is conceivable that *L. pneumophila* Philadelphia-1 JR32 requires more time to cause the disease than the Corby strain, which appears more virulent in previous studies as well as in the HLTE infection model.

6.2.2 Effects of *L. pneumophila* on human lung tissue explants

Pathologic case reports of Legionnaires' disease describe *L. pneumophila* to be found predominantly in alveolar phagocytes; and *in vitro* studies showed the pathogen to transmigrate through a barrier of lung epithelial cells (Glavin *et al.*, 1979; Wagner *et al.*, 2007). In HLTEs, *L. pneumophila* can indeed be detected at two predominant sites, in and on alveolar macrophages and in the connective tissue, underlining the validity of the model. Moreover, bacteria were also detected on alveolar surfaces at early time points, while they tended to cluster on and in alveolar macrophages with increasing time after infection. This suggests that the extracellular alveolar surface represents the initial binding site for *L. pneumophila* in the human lung, whereas the invasion of macrophages occurs only subsequently. The sequence of events during the onset of infection in human was not known before.

In addition, bacteria located close to the connective tissue point towards an important phenotype of Legionnaires' disease – the strong damage to infected tissues. The damage observed in *L. pneumophila*-infected HLTEs can be classified in three types. Protein exudate appeared in alveolar lumina, alveolar epithelia delaminated from the connective tissue and the interalveolar septa were disrupted. Importantly, the damage observed in this study is in concordance with findings in autopsy samples from patients with legionellosis (Glavin *et al.*, 1979; Weisenburger *et al.*, 1981; Winn *et al.*, 1981).

The exact reasons for the observed damage phenotypes remain unclear. The protein-rich exudate in alveolar lumina may be related to a difference in blood vessel permeability, potentially linked to the previously observed colonization of endothelia

by *L. pneumophila* (Chiaraviglio *et al.*, 2008). The disaggregation of connective tissue, e.g. in alveolar septa, may be caused by bacterial enzymes, such as the abundant secreted zinc-dependent protease ProA, or by host proteins which are released by phagocytes or dying cells. It also remains to be elucidated which activities cause epithelial cells to detach from the basal lamina. The latter two types of damage, however, are likely to enable the dissemination of the infection from one alveolus to a neighboring one and, eventually, into the bloodstream, from where *L. pneumophila* can colonize extrapulmonary organs (Watts *et al.*, 1980; Hambleton *et al.*, 1982; Theaker *et al.*, 1987).

An infection of human lung tissue with a DotA-deficient *L. pneumophila* strain results in much weaker damage compared to infections with the wild type. There are two possible explanations for this. Firstly, since the mutant strain does not replicate markedly in HLTEs, there are fewer bacteria present in the respective samples. This results in lower amounts of degradative bacterial enzymes which could destroy the tissue, and potentially in a less intense inflammatory response of the tissue, which can also lead to tissue damage. Secondly, the type IVB secretion-deficient strain may actually cause less tissue damage *per se*. The transcriptional response of infected host cells depends on the respective *L. pneumophila* strain (Losick *et al.*, 2006). This may result in a decreased synthesis of destructive proteins and other molecules by the host, but would not directly depend on the amount of bacteria present.

6.2.3 Tissue damage caused by *L. pneumophila* OMVs

It is unknown if and how OMVs contribute to the course of infection with *L. pneumophila* in general and to the damage to host tissues in particular. To investigate this question, HLTEs were stimulated with purified *L. pneumophila* OMVs over 48 h hours. Subsequently, the damage to the samples was categorized and quantified.

Incubation of tissue samples with OMVs led to damage patterns and intensities comparable to the outcome of an infection with wild type *L. pneumophila*. Additionally, the intensity of the three damage phenotypes is largely similar between infected and OMV-stimulated tissue. This finding shows that OMVs mediate the observed damage after infection at least partially. This hypothesis is supported by the

previous proteomic characterization of OMVs, which revealed large numbers of proteolytic and lipolytic enzymes (Galka *et al.*, 2008). These enzymes could cleave molecules in the connective tissue, including collagen. They may also be involved in the detachment of epithelial cells by cleaving focal adhesion molecules, i.e. integrins. By degrading interalveolar septa, OMVs are likely to contribute to the dissemination of *L. pneumophila* infections from one alveolus to another and from the lung to other organs.

It is important to note that the localization of OMVs in lung tissue is not identical to that of *L. pneumophila* cells. The pathogen adheres to the alveolar lining as well as macrophages and the connective tissue. OMVs on the other hand can be detected predominantly on and in alveolar macrophages, and bind to components of the connective tissue to a lower extent. This indicates that the binding of *L. pneumophila* to connective tissue and the alveolar lining is enhanced by a factor, probably a surface protein, which is not present on OMVs. As a consequence, the collagen-binding protein Mip is not independently responsible for the binding of *L. pneumophila* to the human lung surface, since this protein was also detected in OMVs (Galka *et al.*, 2008). The additional surface molecules which mediate adhesion of *L. pneumophila* to the alveolar lining are to be determined by testing mutant strains deficient in candidate proteins in HLTEs in future experiments.

Seeing the effects of wild type *L. pneumophila* on human lung tissue in the first days after infection, it seems likely that the tissue damage and bacterial dissemination will increase even further in the following days as the pathogen continues to replicate. This cannot be studied in the described infection model yet. However, OMV-stimulated tissue is likely to recover more quickly, since the vesicles will be degraded over time, but no bacteria are present to produce more vesicles. If OMVs lead to severe, but temporary damage to pulmonary tissue, it is conceivable that they are also involved in the pathogenesis of Pontiac fever, whose details remain unclear so far. This assumption is supported by the hypothesis that *Legionella* LPS, but not whole bacterial cells, is the causative agent of Pontiac fever (Fields *et al.*, 2001).

6.2.4 Transcriptional response of infected lung tissue

HLTEs also enable the characterization of the tissue response to infection on the molecular level. To this end, RNA was extracted from infected and uninfected samples to compare their transcriptional profiles. All in all, 2499 genes were identified to be regulated differentially 24 h after infection with wild type *L. pneumophila*. A group of eight Gene Ontology terms is significantly enriched, most notably extracellular proteins and components of the immune system. Interestingly, lipoprotein transport proteins are also enriched among the infection-regulated genes. This suggests an involvement of host lipoprotein and lipid metabolism during infection and can be analyzed in future studies.

The amount of uteroglobin mRNA is strongly increased 24 h after infection with *L. pneumophila*. Uteroglobin, also termed Clara cell secretory protein (CCSP), CC-10, CC-16 or blastokinin, is protein with an unknown molecular function. It is a major constituent of the extracellular lining fluid of the airways (Singh *et al.*, 1990). Uteroglobin is reported to inhibit phospholipase A2 activity and, consequently, immune cell recruitment *in vitro* and after infection of mice with the pulmonary pathogen *P. aeruginosa* (Schiffmann *et al.*, 1983; Levin *et al.*, 1986; Vasanthakumar *et al.*, 1988; Hayashida *et al.*, 2000). Stimulating lung epithelial cells with *P. aeruginosa* or TNF-α results in a decrease in uteroglobin on the mRNA and protein levels (Hayashida *et al.*, 2000; Harrod *et al.*, 2002). The role of uteroglobin in *L. pneumophila* infections has not been described before.

It is conceivable that the pathogen induces upregulation of this protein to prevent the recruitment of neutrophils, which are important for the clearance of *L. pneumophila* infections. The upregulation could not be confirmed on the protein level by immunohistochemistry. It is conceivable that this secreted protein is lost during washing steps of the tissue samples. Alternatively, posttranscriptional or posttranslational events could prevent uteroglobin protein levels to increase, potentially as a result of host-instigated regulation.

The downregulation of MARCO, the macrophage receptor with collagenous structure, after an infection with *L. pneumophila* is striking. MARCO has been reported to serve as a class A scavenger receptor involved in the uptake of the bacterial pathogens *Neisseria meningitidis, Clostridium sordellii* and *Streptococcus mutans* (Elomaa *et al.*,

1995; Elomaa *et al.*, 1998; Mukhopadhyay *et al.*, 2006; Thelen *et al.*, 2010; Braun *et al.*, 2011; Mukouhara *et al.*, 2011). Interestingly, this protein is also involved in the modulation of cytokine responses to infections with *Mycobacterium tuberculosis* and influenza A virus (Bowdish *et al.*, 2009; Ghosh *et al.*, 2011). It seems unlikely that *L. pneumophila* would actively suppress the synthesis of a protein involved in the uptake of bacteria, since its replication depends on this process. Future experiments can further elucidate the role of MARCO, a new player in *L. pneumophila*-host interactions.

On a side note, the phagocytosis of *S. mutans* is partially mediated by MARCO, and the pathogen suppresses this function with a peptidyl-prolyl *cis-trans* isomerase (Mukouhara *et al.*, 2011). *L. pneumophila* also features a virulence factor with this enzymatic activity, Mip, whose molecular function during infections has not been clarified; but Mip-deficient mutants are less effective in initiating invasion in macrophages (Cianciotto *et al.*, 1989). It is conceivable that Mip also modulates the function of MARCO. Given that MARCO has an extracellular collagenous domain and that Mip binds to collagen IV (Wagner *et al.*, 2007), an interaction between these two proteins is probable. The synthetic peptide P290, whose sequence was derived from collagen IV, binds specifically to the active site of *L. pneumophila* Mip (Ünal *et al.*, 2011). The alignment of human collagen IV, MARCO and P290 reveals a weak consensus sequence (Figure 18). In particular, the collagen-like domain of MARCO features two identical and four conserved residues compared to P290. If Mip actually binds MARCO *in vivo* can be determined in future studies.

```
collagen        CAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWIGYSFVMHTSAGAEGSGQALASPGSCLEE
MARCO           ----------MLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLWSCTKNSWGHHDCSHE
P290            -------------------IPPCPSGWSSLWI----------------------------
                                    :    :* ..:*:
```

Figure 18: Multiple sequence alignment of human collagen IV, the collagenous domain of MARCO and the Mip-binding peptide P290 performed on http://www.genome.jp/tools/clustalw. *****: fully conserved residue, **:**: strong similarity, **.**: weak similarity.

Bearing in mind that Mip-negative strains do not display defects in adhesion to host cells (Cianciotto *et al.*, 1989), it is possible that signaling events induced by the potential Mip-MARCO interaction, but not the binding itself, are required for the successful establishment of an infection with *L. pneumophila*. In response to an

infection with this pathogen, macrophages might reactively reduce MARCO levels in order to weaken the initiation of intracellular replication.

Studying the transcriptional profile of tissue stimulated with *L. pneumophila* OMVs will be particularly interesting. While OMVs do not influence the quantitative outcome of infection in human macrophages on the cellular level, they do elicit a specific cytokine response from alveolar epithelial cells (Galka *et al.*, 2008). This includes the secretion of pro-inflammatory cytokines which recruit phagocytes to sites of infection, such as IL-6, IL-8 and MCP-1, but also IL-13, whose secretion is specifically induced by *L. pneumophila* OMVs. Interestingly, IL-13 promotes the synthesis of several matrix metalloproteases and cathepsins which contribute to lung tissue damage in emphysema and potentially Legionnaires' disease (Zheng *et al.*, 2000). Thus, *L. pneumophila* OMVs may directly damage the extracellular matrix via their destructive enzymes and indirectly via the induction of host enzymes. As a consequence, OMVs are likely to contribute to the destruction of the affected tissue and the dissemination of the infection from the human lung to other organs.

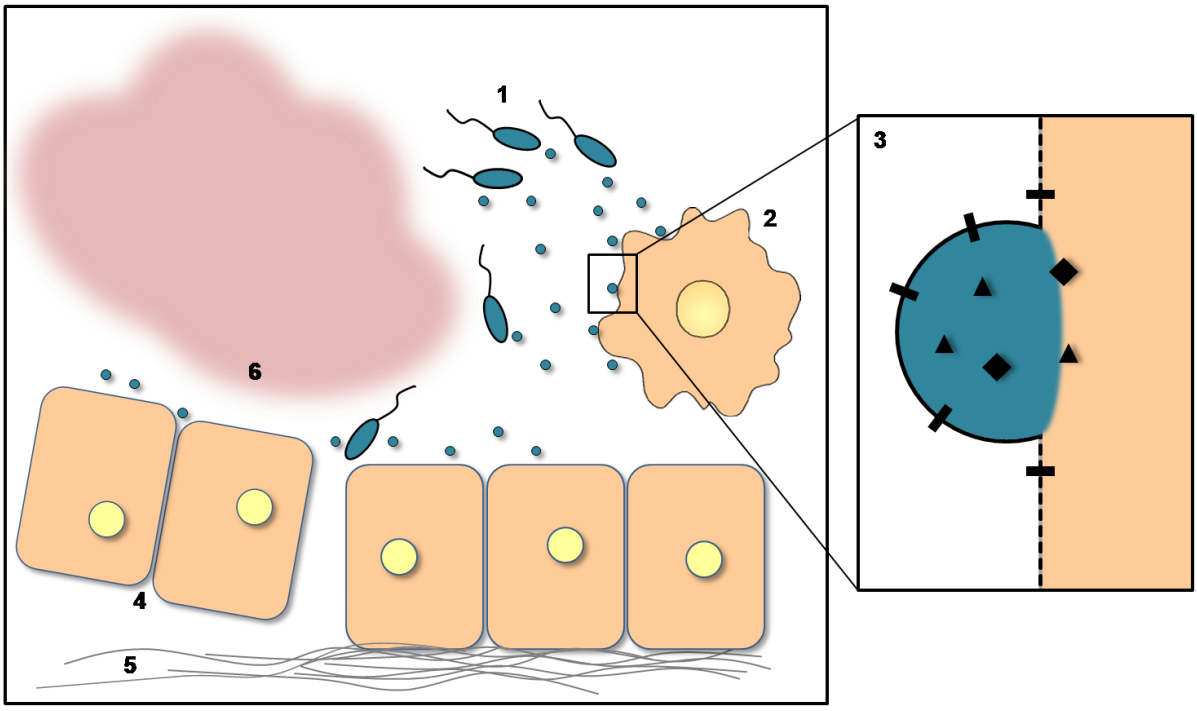

Figure 19: Overview of the functions of *L. pneumophila* OMVs observed in this work. The pathogen produces vesicles during infections of human alveoli (1). The OMVs associate with the surface of alveolar macrophages (2), with whose plasma membrane they fuse (3), thereby delivering cargo into the macrophage cytosol. A mixed phase of bacterial and eukaryotic lipids is formed which includes membrane components from *L. pneumophila*. Potentially, OMVs also fuse with other, intracellular

membranes. Additionally, *L. pneumophila* and its OMVs induce the detachment of alveolar epithelia (4), the disintegration of the pulmonary connective tissue (5) and the formation of protein exudate in the alveolar lumen (6).

6.3 Outlook

While the fusion of *L. pneumophila* OMVs with host membranes is probable, the exact subcellular targets can be identified by colocalization studies with markers for individual compartments. In addition to these effects on the cellular level, the influence of OMVs on the pathogenesis of Legionnaires' disease appears to be focused in cell complexes and tissues. Experiments with OMVs from mutant strains can show which enzymes are involved in the degradation of lung tissue, and which OMV components are required for the characteristic cytokine response. Assessing effects of *L. pneumophila* OMVs on human lung tissue on the molecular level will answer more questions on their role in the virulence of this pathogen.

Studying *L. pneumophila* infections in human lung tissue explants is an extremely promising approach. It allows for the characterization of early events in the pathogenesis of Legionnaires' disease, such as initial contact between the pathogen and host structures, from the tissue architecture down to the molecular level. Electron microscopy can elucidate subcellular events in the infected tissue. Experiments with *L. pneumophila* mutant strains can help to evaluate the role of individual genes and their gene products by analyzing bacterial replication, tissue damage after infection and the transcriptional response of the tissue. Promising candidate proteins include the aforementioned metalloprotease ProA, which is likely to contribute to tissue degradation, and the PPIase Mip, which binds collagen and was reported to contribute to the transmigration of *L. pneumophila* through epithelial layers (Wagner *et al.*, 2007). Preliminary studies have already shown that ProA damages the pulmonary tissue architecture, while Mip does not induce visible damage. Further characterization of the effect of these proteins, as well as *L. pneumophila* strains deficient in Mip and ProA, will show their involvement in the degradation of the connective tissue and the localization of the pathogen to host structures.

Moreover, the transcriptional profile of the pathogen itself can be analyzed after careful extraction of bacterial RNA from infected tissue samples. These experiments can shed light on the adaptation of *L. pneumophila* to the lung environment,

particularly in comparison to the transcriptional studies on *L. pneumophila* within macrophages *in vitro* (Faucher *et al.*, 2011). Among the genes differentially regulated in human tissue, new virulence factors may be identified.

Previous studies showed that *L. pneumophila* invasion and intracellular replication in mammalian cells are strongly enhanced if the bacteria were not grown on laboratory media, but are harvested from infected protozoa (Cirillo *et al.*, 1994; Cirillo *et al.*, 1999). Co-infection with *L. pneumophila* and *H. vermiformis* increased the histological damage to murine lungs and modified the immune response compared to infection with the bacterium alone (Brieland *et al.*, 1996). It will be interesting to study if and how a pre-infection of amoebae also influences the course of infection in human lung tissue, since *L. pneumophila*-infected amoebae increase the infectivity of the pathogen and are discussed to transfer it to humans from contaminated devices (Brieland *et al.*, 1997; Singh *et al.*, 2005). In addition to the physiological and morphological changes induced by infection of amoebae, infected protozoa may also carry a sufficient number of *L. pneumophila* to cause Legionnaires' disease (Singh *et al.*, 2005). To address this question, lung tissue samples can be infected with suspensions of *L. pneumophila*-infected amoeba, e.g. *H. vermiformis* or *A. castellanii,* and the appropriate controls to analyze the histology and bacterial replication.

Furthermore, HTLEs can also be applied to study infections with other pathogens, including Gram-positive bacteria and viruses affecting the human lung. Optimization of the protocols may be required, but could lead to similarly intriguing results as this study on *L. pneumophila*.

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8. Appendix

8.1. Abbreviations

DMPC	1,2-Dimyristoyl-*sn*-glycero-3-phosphocholine
ER	Endoplasmic reticulum
FC	Fold change
HLTE	Human lung tissue explant
IFN	Interferon
IL	Interleukin
LCV	*Legionella*-containing vacuole
LPS	Lipopolysaccharide
MCP-1	Macrophage chemoattractant protein 1
MOI	Multiplicity of infection
OD_{600}	Optical density at 600 nm
OM	Outer membrane
OMV	Outer membrane vesicle
PC	Phosphatidylcholine
PE	Phosphatidylethanolamine
PLMAK	Phospholipid mixture mimicking the lipid composition of macrophage (Kröner *et al.,* 1981)
POPS	1-Palmitoyl-2-oleoyl-*sn*-glycero-3-(phospho-L-serine)
PQS	*Pseudomonas* quinolone signal
PS	Phosphatidylserine
SNARE	SNAP (Soluble N-ethylmaleimide-sensitive factor Attachment Protein) REceptor
S. Typhimurium	*Salmonella enterica* ssp. *enterica* serovar Typhimurium
Wt	Wild type

8.2. Transcriptonal response of HLTEs to *L. pneumophila*

Table A1: List of differentially regulated genes after infection of human lung tissue explants with wildtype *L. pneumophila* Corby after 24 h. Only genes with > two-fold change (FC) are listed; n = 2.

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1	A_24_P149902	42,843	up	SUFU	Homo sapiens suppressor of fused homolog (Drosophila) (SUFU), transcript variant 1, mRNA [NM_016169]
2	A_33_P3246028	12,547	up	DCDC2B	Homo sapiens doublecortin domain containing 2B (DCDC2B), mRNA [NM_001099434]
3	A_33_P3332406	12,511	up	LDLRAD1	Homo sapiens low density lipoprotein receptor class A domain containing 1 (LDLRAD1), mRNA [NM_001010978]
4	A_23_P312300	11,882	up	SCGB2A1	Homo sapiens secretoglobin, family 2A, member 1 (SCGB2A1), mRNA [NM_002407]
5	A_33_P3220207	11,475	up	ARMC3	Homo sapiens armadillo repeat containing 3 (ARMC3), mRNA [NM_173081]
6	A_23_P61031	11,454	up	ZBBX	Homo sapiens zinc finger, B-box domain containing (ZBBX), transcript variant 2, mRNA [NM_024687]
7	A_24_P491397	11,215	up	LDLRAD1	Homo sapiens low density lipoprotein receptor class A domain containing 1 (LDLRAD1), mRNA [NM_001010978]
8	A_23_P139146	10,917	up	MS4A8B	Homo sapiens membrane-spanning 4-domains, subfamily A, member 8B (MS4A8B), mRNA [NM_031457]
9	A_23_P426153	10,116	up	CCDC37	Homo sapiens coiled-coil domain containing 37 (CCDC37), mRNA [NM_182628]
10	A_23_P86540	10,018	up	ARMC3	Homo sapiens armadillo repeat containing 3 (ARMC3), mRNA [NM_173081]
11	A_24_P401491	9,922	up	MORN5	Homo sapiens MORN repeat containing 5 (MORN5), mRNA [NM_198469]
12	A_33_P3261054	9,818	up	CCDC114	Homo sapiens coiled-coil domain containing 114 (CCDC114), transcript variant 2, mRNA [NM_144577]
13	A_23_P2052	9,368	up	MMP26	Homo sapiens matrix metallopeptidase 26 (MMP26), mRNA [NM_021801]
14	A_32_P85106	9,279	up	C6orf118	Homo sapiens chromosome 6 open reading frame 118 (C6orf118), mRNA [NM_144980]
15	A_24_P522998	9,096	up	C1orf173	Homo sapiens chromosome 1 open reading frame 173 (C1orf173), mRNA [NM_001002912]
16	A_23_P218047	8,983	up	KRT5	Homo sapiens keratin 5 (KRT5), mRNA [NM_000424]
17	A_23_P77918	8,877	up	HS3ST3B1	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA [NM_006041]
18	A_23_P353056	8,650	up	C2CD2L	Homo sapiens C2CD2-like (C2CD2L), mRNA [NM_014807]
19	A_23_P346912	8,485	up	SPATA17	Homo sapiens spermatogenesis associated 17 (SPATA17), mRNA [NM_138796]
20	A_33_P3288357	8,334	up	C9orf117	chromosome 9 open reading frame 117 [Source:HGNC Symbol;Acc:27843] [ENST00000373293]
21	A_23_P107775	7,710	up	TMEM190	Homo sapiens transmembrane protein 190 (TMEM190), mRNA [NM_139172]
22	A_24_P165545	7,580	up	TTLL10	Homo sapiens tubulin tyrosine ligase-like family, member 10 (TTLL10), transcript variant 2, mRNA [NM_153254]
23	A_33_P3244643	7,529	up	FAM183A	Homo sapiens family with sequence similarity 183, member A (FAM183A), mRNA [NM_001101376]
24	A_33_P3291244	7,440	up	CCDC60	Homo sapiens coiled-coil domain containing 60 (CCDC60), mRNA [NM_178499]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
25	A_23_P501933	7,288	up	CACNG6	Homo sapiens calcium channel, voltage-dependent, gamma subunit 6 (CACNG6), transcript variant 1, mRNA [NM_145814]
26	A_23_P308722	7,133	up	CCDC164	Homo sapiens coiled-coil domain containing 164 (CCDC164), mRNA [NM_145038]
27	A_24_P229638	7,000	up	C9orf117	Homo sapiens chromosome 9 open reading frame 117 (C9orf117), mRNA [NM_001012502]
28	A_23_P314835	6,946	up	C20orf85	Homo sapiens chromosome 20 open reading frame 85 (C20orf85), mRNA [NM_178456]
29	A_32_P204239	6,891	up	CDHR3	Homo sapiens cadherin-related family member 3 (CDHR3), mRNA [NM_152750]
30	A_23_P8702	6,832	up	PIP	Homo sapiens prolactin-induced protein (PIP), mRNA [NM_002652]
31	A_24_P391991	6,804	up	FAM183B	Homo sapiens family with sequence similarity 183, member B (FAM183B), non-coding RNA [NR_028347]
32	A_23_P140009	6,756	up	SLC10A2	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA [NM_000452]
33	A_23_P386384	6,730	up	C1orf87	Homo sapiens chromosome 1 open reading frame 87 (C1orf87), mRNA [NM_152377]
34	A_33_P3241661	6,595	up	LOC388780	PREDICTED: Homo sapiens hypothetical LOC388780 (LOC388780), partial miscRNA [XR_109642]
35	A_33_P3384552	6,575	up	LOC388553	PREDICTED: Homo sapiens hypothetical LOC388553 (LOC388553), mRNA [XM_373809]
36	A_23_P357983	6,461	up	STOML3	Homo sapiens stomatin (EPB72)-like 3 (STOML3), transcript variant 1, mRNA [NM_145286]
37	A_23_P80200	6,453	up	LOC400891	Homo sapiens chromosome 14 open reading frame 166B pseudogene (LOC400891), non-coding RNA [NR_027006]
38	A_33_P3292387	6,363	up	LRRIQ3	Homo sapiens leucine-rich repeats and IQ motif containing 3 (LRRIQ3), mRNA [NM_001105659]
39	A_33_P3286349	6,321	up	C19orf51	Homo sapiens chromosome 19 open reading frame 51 (C19orf51), mRNA [NM_178837]
40	A_33_P3288871	6,256	up	SLC38A1	solute carrier family 38, member 1 [Source:HGNC Symbol;Acc:13447] [ENST00000550173]
41	A_23_P164068	6,230	up	DNAH9	Homo sapiens dynein, axonemal, heavy chain 9 (DNAH9), transcript variant 2, mRNA [NM_001372]
42	A_24_P286951	6,202	up	C10orf81	Homo sapiens chromosome 10 open reading frame 81 (C10orf81), transcript variant 4, mRNA [NM_024889]
43	A_33_P3318946	6,193	up	HAPLN2	Homo sapiens hyaluronan and proteoglycan link protein 2 (HAPLN2), mRNA [NM_021817]
44	A_32_P74579	6,164	up	GAS2L2	Homo sapiens growth arrest-specific 2 like 2 (GAS2L2), mRNA [NM_139285]
45	A_23_P92120	6,126	up	SNTN	Homo sapiens sentan, cilia apical structure protein (SNTN), mRNA [NM_001080537]
46	A_23_P217009	6,102	up	C9orf24	Homo sapiens chromosome 9 open reading frame 24 (C9orf24), transcript variant 1, mRNA [NM_032596]
47	A_32_P35947	6,075	up		
48	A_33_P3304242	6,067	up	DNAI1	Homo sapiens dynein, axonemal, intermediate chain 1 (DNAI1), mRNA [NM_012144]
49	A_23_P20578	6,030	up	FAM166B	Homo sapiens family with sequence similarity 166, member B (FAM166B), transcript variant 1, mRNA [NM_001164310]
50	A_33_P3418234	6,003	up		Homo sapiens beclin 2 (BECN2) mRNA, complete cds, [HM031116]
51	A_33_P3707547	5,964	up	LOC541467	Homo sapiens hypothetical LOC541467, mRNA (cDNA clone IMAGE:4830703), partial cds, [BC045815]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
52	A_33_P3415625	5,881	up	LRRIQ1	Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA [NM_001079910]
53	A_33_P3477521	5,860	up	LOC284080	Homo sapiens hypothetical LOC284080 (LOC284080), non-coding RNA [NR_038230]
54	A_33_P3318449	5,828	up	RNF222	Homo sapiens ring finger protein 222 (RNF222), mRNA [NM_001146684]
55	A_33_P3309832	5,746	up	C10orf81	Homo sapiens chromosome 10 open reading frame 81 (C10orf81), transcript variant 1, mRNA [NM_182601]
56	A_23_P212258	5,712	up	KNG1	Homo sapiens kininogen 1 (KNG1), transcript variant 2, mRNA [NM_000893]
57	A_23_P102950	5,673	up	RSPH1	Homo sapiens radial spoke head 1 homolog (Chlamydomonas) (RSPH1), mRNA [NM_080860]
58	A_23_P93141	5,657	up	GSTA5	Homo sapiens glutathione S-transferase alpha 5 (GSTA5), mRNA [NM_153699]
59	A_33_P3806704	5,565	up	LOC100129198	Homo sapiens clone FLC0664 PRO2866 mRNA, complete cds, [AF130117]
60	A_33_P3352906	5,562	up	NCRNA00099	Homo sapiens non-protein coding RNA 99 (NCRNA00099), non-coding RNA [NR_002813]
61	A_23_P401055	5,540	up	SOX2	Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA [NM_003106]
62	A_33_P3401586	5,521	up	EFCAB10	Homo sapiens EF-hand calcium binding domain 10 (EFCAB10), non-coding RNA [NR_027068]
63	A_33_P3229107	5,518	up	LOC642587	Homo sapiens NPC-A-5 (LOC642587), mRNA [NM_001104548]
64	A_33_P3343972	5,517	up	RSPH1	Homo sapiens radial spoke head 1 homolog (Chlamydomonas) (RSPH1), mRNA [NM_080860]
65	A_33_P3271166	5,500	up	OR6C74	Homo sapiens olfactory receptor, family 6, subfamily C, member 74 (OR6C74), mRNA [NM_001005490]
66	A_24_P289299	5,497	up	ARHGEF25	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 25 (ARHGEF25), transcript variant 1, mRNA [NM_182947]
67	A_23_P75063	5,481	up	DYDC2	Homo sapiens DPY30 domain containing 2 (DYDC2), mRNA [NM_032372]
68	A_33_P3404453	5,462	up	AOX2P	Homo sapiens aldehyde oxidase 2 pseudogene (AOX2P), non-coding RNA [NR_001557]
69	A_33_P3785051	5,454	up	EFCAB10	Homo sapiens cDNA clone IMAGE:6616931, partial cds, [BC062748]
70	A_23_P348253	5,439	up	CDHR3	Homo sapiens cadherin-related family member 3 (CDHR3), mRNA [NM_152750]
71	A_23_P312999	5,412	up	C4orf22	Homo sapiens chromosome 4 open reading frame 22 (C4orf22), transcript variant 2, mRNA [NM_152770]
72	A_33_P3396537	5,400	up	CDHR4	Homo sapiens cadherin-related family member 4 (CDHR4), mRNA [NM_001007540]
73	A_32_P15512	5,389	up	C1orf194	Homo sapiens chromosome 1 open reading frame 194 (C1orf194), mRNA [NM_001122961]
74	A_23_P383679	5,361	up	HYDIN	Homo sapiens hydrocephalus inducing homolog (mouse) (HYDIN), transcript variant 1, mRNA [NM_032821]
75	A_24_P313993	5,333	up	CAPS	Homo sapiens calcyphosine (CAPS), transcript variant 1, mRNA [NM_004058]
76	A_33_P3354847	5,273	up	C9orf171	Homo sapiens chromosome 9 open reading frame 171 (C9orf171), mRNA [NM_207417]
77	A_23_P132826	5,180	up	SERPINI2	Homo sapiens serpin peptidase inhibitor, clade I (pancpin), member 2 (SERPINI2), mRNA [NM_006217]
78	A_23_P386268	5,162	up	C4orf26	Homo sapiens chromosome 4 open reading frame 26 (C4orf26), transcript variant 2, mRNA [NM_178497]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
79	A_23_P2322	5,158	up	TSPAN19	Homo sapiens tetraspanin 19 (TSPAN19), mRNA [NM_001100917]
80	A_33_P3261586	5,155	up	CCDC108	Homo sapiens coiled-coil domain containing 108 (CCDC108), transcript variant 1, mRNA [NM_194302]
81	A_23_P333038	5,153	up	WDR96	Homo sapiens WD repeat domain 96 (WDR96), mRNA [NM_025145]
82	A_23_P33583	5,107	up	DNAH7	Homo sapiens dynein, axonemal, heavy chain 7 (DNAH7), mRNA [NM_018897]
83	A_33_P3272429	5,087	up	CCDC126	coiled-coil domain containing 126 [Source:HGNC Symbol;Acc:22398] [ENST00000472407]
84	A_32_P489986	5,081	up	TMEM232	Homo sapiens transmembrane protein 232 (TMEM232), mRNA [NM_001039763]
85	A_23_P92928	5,064	up	C6	Homo sapiens complement component 6 (C6), transcript variant 1, mRNA [NM_000065]
86	A_33_P3349025	5,058	up		
87	A_23_P115780	5,035	up	LRIT1	Homo sapiens leucine-rich repeat, immunoglobulin-like and transmembrane domains 1 (LRIT1), mRNA [NM_015613]
88	A_33_P3244112	5,020	up	UOX	Homo sapiens urate oxidase, pseudogene (UOX), non-coding RNA [NR_003927]
89	A_33_P3422010	5,020	up	DNAH12	Homo sapiens dynein, axonemal, heavy chain 12 (DNAH12), transcript variant 1, mRNA [NM_178504]
90	A_23_P114353	4,986	up	NXF5	Homo sapiens nuclear RNA export factor 5 (NXF5), transcript variant 1, mRNA [NM_032946]
91	A_24_P262321	4,952	up	FAM18B2-CDRT4	Homo sapiens FAM18B2-CDRT4 readthrough (FAM18B2-CDRT4), transcript variant 1, mRNA [NM_001204478]
92	A_33_P3293362	4,904	up	MOSC1	Homo sapiens MOCO sulphurase C-terminal domain containing 1 (MOSC1), nuclear gene encoding mitochondrial protein, mRNA [NM_022746]
93	A_23_P4074	4,858	up	WDR16	Homo sapiens WD repeat domain 16 (WDR16), transcript variant 2, mRNA [NM_145054]
94	A_24_P943370	4,846	up	GAGE1	Homo sapiens G antigen 1 (GAGE1), transcript variant 1, mRNA [NM_001468]
95	A_23_P45955	4,823	up	TEKT2	Homo sapiens tektin 2 (testicular) (TEKT2), mRNA [NM_014466]
96	A_23_P133536	4,797	up	CAPSL	Homo sapiens calcyphosine-like (CAPSL), transcript variant 1, mRNA [NM_144647]
97	A_33_P3370707	4,783	up	CRX	Homo sapiens cone-rod homeobox (CRX), mRNA [NM_000554]
98	A_33_P3218490	4,783	up	LOC100128226	Homo sapiens mRNA for hypothetic protein, complete cds, Alzheimer disease site specific expressed gene, [AB128931]
99	A_33_P3284888	4,769	up	DLEU7	Homo sapiens deleted in lymphocytic leukemia, 7 (DLEU7), mRNA [NM_198989]
100	A_33_P3617190	4,765	up	LOC651337	Homo sapiens cDNA FLJ42125 fis, clone TESTI2009511, [AK124119]
101	A_33_P3328716	4,764	up	CCDC13	Homo sapiens coiled-coil domain containing 13 (CCDC13), mRNA [NM_144719]
102	A_33_P3302185	4,756	up	HS3ST6	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 6 (HS3ST6), mRNA [NM_001009606]
103	A_23_P313652	4,752	up	AKAP14	Homo sapiens A kinase (PRKA) anchor protein 14 (AKAP14), transcript variant 1, mRNA [NM_178813]
104	A_24_P340954	4,734	up	ANKUB1	Homo sapiens ankyrin repeat and ubiquitin domain containing 1 (ANKUB1), mRNA [NM_001144960]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
105	A_33_P3396858	4,729	up		
106	A_23_P152949	4,720	up	LRRC46	Homo sapiens leucine rich repeat containing 46 (LRRC46), mRNA [NM_033413]
107	A_23_P426944	4,718	up	PAX9	Homo sapiens paired box 9 (PAX9), mRNA [NM_006194]
108	A_33_P3238895	4,704	up		Homo sapiens PNAS-17 mRNA, complete cds, [AF274942]
109	A_23_P255876	4,700	up	DNAI1	Homo sapiens dynein, axonemal, intermediate chain 1 (DNAI1), mRNA [NM_012144]
110	A_33_P3295313	4,685	up	MS4A2	Homo sapiens membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) (MS4A2), mRNA [NM_000139]
111	A_33_P3380076	4,684	up	LOC100131673	PREDICTED: Homo sapiens hypothetical protein LOC100131673 (LOC100131673), mRNA [XM_001723856]
112	GE_BrightCorner	4,674	up		Unknown
113	A_32_P4262	4,631	up	C20orf26	Homo sapiens chromosome 20 open reading frame 26 (C20orf26), transcript variant 1, mRNA [NM_015585]
114	A_33_P3218699	4,621	up	MDH1B	Homo sapiens malate dehydrogenase 1B, NAD (soluble) (MDH1B), mRNA [NM_001039845]
115	A_33_P3366132	4,617	up		Q5U635_HUMAN (Q5U635) SEMA6A protein, partial (10%) [THC2690044]
116	A_23_P414281	4,601	up	C16orf71	Homo sapiens chromosome 16 open reading frame 71 (C16orf71), mRNA [NM_139170]
117	A_23_P18282	4,597	up	DLEC1	Homo sapiens deleted in lung and esophageal cancer 1 (DLEC1), transcript variant DLEC1-N1, mRNA [NM_007335]
118	A_23_P367071	4,583	up	UBE2DNL	Homo sapiens ubiquitin-conjugating enzyme E2D N-terminal like (pseudogene) (UBE2DNL), non-coding RNA [NR_024062]
119	A_33_P3236778	4,582	up		
120	A_23_P319783	4,578	up	SPAG17	Homo sapiens sperm associated antigen 17 (SPAG17), mRNA [NM_206996]
121	A_23_P89981	4,545	up	CYP2F1	Homo sapiens cytochrome P450, family 2, subfamily F, polypeptide 1 (CYP2F1), mRNA [NM_000774]
122	A_23_P145711	4,535	up	C7orf10	Homo sapiens chromosome 7 open reading frame 10 (C7orf10), transcript variant 4, mRNA [NM_024728]
123	A_23_P150583	4,531	up	SCGB1A1	Homo sapiens secretoglobin, family 1A, member 1 (uteroglobin) (SCGB1A1), mRNA [NM_003357]
124	A_33_P3278877	4,530	up	ROBO2	Homo sapiens roundabout, axon guidance receptor, homolog 2 (Drosophila) (ROBO2), transcript variant 2, mRNA [NM_002942]
125	A_32_P167705	4,515	up	AGBL2	Homo sapiens ATP/GTP binding protein-like 2 (AGBL2), mRNA [NM_024783]
126	A_23_P417261	4,509	up	EFHB	Homo sapiens EF-hand domain family, member B (EFHB), mRNA [NM_144715]
127	A_32_P225345	4,486	up	C11orf88	Homo sapiens chromosome 11 open reading frame 88 (C11orf88), transcript variant 1, mRNA [NM_207430]
128	A_33_P3314643	4,483	up	SPEF1	Homo sapiens sperm flagellar 1 (SPEF1), mRNA [NM_015417]
129	A_24_P374973	4,451	up		
130	A_23_P71379	4,447	up	PSCA	Homo sapiens prostate stem cell antigen (PSCA), transcript variant 1, mRNA [NM_005672]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
131	A_33_P3297626	4,425	up	KIAA0090	KIAA0090 [Source:HGNC Symbol;Acc:28957] [ENST00000356068]
132	A_33_P3249076	4,403	up	HOGA1	4-hydroxy-2-oxoglutarate aldolase 1 [Source:HGNC Symbol;Acc:25155] [ENST00000465608]
133	A_33_P3482466	4,394	up		Homo sapiens cDNA FLJ37235 fis, clone BRAMY2002525, [AK094554]
134	A_33_P3415596	4,385	up	LOC400499	PREDICTED: Homo sapiens hypothetical protein LOC400499 (LOC400499), mRNA [XM_003118689]
135	A_33_P3424204	4,371	up	DLEU2L	Homo sapiens deleted in lymphocytic leukemia 2-like (DLEU2L), non-coding RNA [NR_002771]
136	A_33_P3265314	4,370	up	FLJ44054	Homo sapiens hypothetical LOC643365 (FLJ44054), non-coding RNA [NR_024609]
137	A_33_P3805839	4,365	up		BC033622 inosine monophosphate dehydrogenase 1, isoform b {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (44%) [THC2568076]
138	A_33_P3422248	4,336	up		nae18g06,x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3435827 3' similar to contains Alu repetitive element;, mRNA sequence [BF733045]
139	A_32_P228268	4,330	up	DNAH10	Homo sapiens dynein, axonemal, heavy chain 10 (DNAH10), mRNA [NM_207437]
140	A_33_P3256287	4,326	up		family with sequence similarity 95, member B1 [Source:HGNC Symbol;Acc:32318] [ENST00000455995]
141	A_33_P3232269	4,320	up	OK/SW-CL,36	Homo sapiens mRNA for OK/SW-CL,36, complete cds, [AB064670]
142	A_24_P268662	4,320	up	ABHD10	Homo sapiens abhydrolase domain containing 10 (ABHD10), mRNA [NM_018394]
143	A_23_P9402	4,308	up	CNTFR	Homo sapiens ciliary neurotrophic factor receptor (CNTFR), transcript variant 1, mRNA [NM_147164]
144	A_33_P3402489	4,307	up	OAS3	Homo sapiens 2'-5'-oligoadenylate synthetase 3, 100kDa (OAS3), mRNA [NM_006187]
145	A_33_P3223488	4,300	up	FRY	Homo sapiens furry homolog (Drosophila) (FRY), mRNA [NM_023037]
146	A_33_P3422025	4,284	up	DNAH12	Homo sapiens dynein, axonemal, heavy chain 12 (DNAH12), transcript variant 1, mRNA [NM_178504]
147	A_24_P257971	4,268	up	SLC27A4	Homo sapiens solute carrier family 27 (fatty acid transporter), member 4 (SLC27A4), mRNA [NM_005094]
148	A_23_P166526	4,240	up	RIBC2	Homo sapiens RIB43A domain with coiled-coils 2 (RIBC2), mRNA [NM_015653]
149	A_33_P3339720	4,218	up	LOC644841	Homo sapiens cDNA FLJ42553 fis, clone BRACE3005225, [AK124544]
150	A_33_P3301034	4,203	up	LRRC28	Homo sapiens leucine rich repeat containing 28 (LRRC28), mRNA [NM_144598]
151	A_23_P348524	4,194	up	C20orf201	Homo sapiens chromosome 20 open reading frame 201 (C20orf201), mRNA [NM_001007125]
152	A_23_P25348	4,180	up	ACAD10	Homo sapiens acyl-CoA dehydrogenase family, member 10 (ACAD10), transcript variant 2, mRNA [NM_025247]
153	A_23_P11980	4,174	up	LOC100509924	PREDICTED: Homo sapiens WD repeat-containing protein 65-like (LOC100509924), mRNA [XM_003119794]
154	A_33_P3315243	4,164	up	C17orf72	Homo sapiens chromosome 17 open reading frame 72 (C17orf72), transcript variant 2, mRNA [NM_001164257]
155	A_32_P112910	4,162	up	UBL4B	Homo sapiens ubiquitin-like 4B (UBL4B), mRNA [NM_203412]
156	A_32_P56624	4,155	up	FAM92B	Homo sapiens family with sequence similarity 92, member B (FAM92B), mRNA [NM_198491]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
157	A_24_P226332	4,145	up	EPHA7	Homo sapiens EPH receptor A7 (EPHA7), mRNA [NM_004440]
158	A_33_P3332414	4,128	up	ABCB1	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 1 (ABCB1), mRNA [NM_000927]
159	A_33_P3286943	4,096	up		
160	A_33_P3258127	4,089	up	LOC100132188	Homo sapiens LP7097 mRNA, complete cds, [AY203946]
161	A_33_P3401452	4,083	up	CHD6	Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA [NM_032221]
162	A_33_P3291034	4,080	up	C1QTNF8	Homo sapiens C1q and tumor necrosis factor related protein 8 (C1QTNF8), mRNA [NM_207419]
163	A_33_P3243118	4,079	up	OR4C6	Homo sapiens olfactory receptor, family 4, subfamily C, member 6 (OR4C6), mRNA [NM_001004704]
164	A_33_P3225066	4,079	up	DNAJC12	Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 12 (DNAJC12), transcript variant 2, mRNA [NM_201262]
165	A_23_P360354	4,078	up	FAM81B	Homo sapiens family with sequence similarity 81, member B (FAM81B), mRNA [NM_152548]
166	A_33_P3706494	4,051	up	LOC284294	Homo sapiens hypothetical LOC284294 (LOC284294), non-coding RNA [NR_033881]
167	A_33_P3419998	4,048	up	SLC4A8	Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8), transcript variant 1, mRNA [NM_001039960]
168	A_32_P138396	4,047	up	LOC100131176	Homo sapiens cDNA FLJ38667 fis, clone HLUNG2006843, [AK095986]
169	A_33_P3239765	4,042	up	LOC100129936	Homo sapiens cDNA FLJ42830 fis, clone BRCAN2017905, [AK124820]
170	A_33_P3617655	4,040	up	LOC339442	Homo sapiens hypothetical LOC339442 (LOC339442), non-coding RNA [NR_038928]
171	A_33_P3221414	4,038	up	NTNG1	netrin G1 [Source:HGNC Symbol;Acc:23319] [ENST00000370068]
172	A_23_P36882	4,029	up	NTS	Homo sapiens neurotensin (NTS), mRNA [NM_006183]
173	A_33_P3329063	4,027	up	NCR1	Homo sapiens natural cytotoxicity triggering receptor 1 (NCR1), transcript variant 1, mRNA [NM_004829]
174	A_23_P393025	4,018	up	SPATA4	Homo sapiens spermatogenesis associated 4 (SPATA4), mRNA [NM_144644]
175	A_33_P3364607	4,017	up	LOC100130051	Homo sapiens cDNA FLJ45363 fis, clone BRHIP3015854, [AK127296]
176	A_23_P94397	4,009	up	OMD	Homo sapiens osteomodulin (OMD), mRNA [NM_005014]
177	A_33_P3312638	3,988	up	ZNF780B	Homo sapiens zinc finger protein 780B (ZNF780B), mRNA [NM_001005851]
178	A_23_P255701	3,983	up	LRRC48	Homo sapiens leucine rich repeat containing 48 (LRRC48), transcript variant 2, mRNA [NM_031294]
179	A_23_P81369	3,967	up	ADAM19	Homo sapiens ADAM metallopeptidase domain 19 (ADAM19), mRNA [NM_033274]
180	A_23_P351328	3,964	up	C2orf53	Homo sapiens chromosome 2 open reading frame 53 (C2orf53), mRNA [NM_178553]
181	A_32_P66756	3,947	up		Glycosyltransferase 54 domain-containing protein [Source:UniProtKB/Swiss-Prot;Acc:A6NG13] [ENST00000513106]
182	A_33_P3329592	3,946	up	BLOC1S3	Homo sapiens biogenesis of lysosomal organelles complex-1, subunit 3 (BLOC1S3), mRNA [NM_212550]
183	A_33_P3219950	3,945	up	LOC729658	Homo sapiens cDNA, FLJ18254, [AK311212]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
184	A_33_P3400688	3,942	up	SLC24A5	Homo sapiens solute carrier family 24, member 5 (SLC24A5), mRNA [NM_205850]
185	A_33_P3267463	3,940	up	RFX3	regulatory factor X, 3 (influences HLA class II expression) [Source:HGNC Symbol;Acc:9984] [ENST00000381984]
186	A_33_P3636257	3,916	up	LOC642345	Homo sapiens hCG1818123 (LOC642345), non-coding RNA [NR_033829]
187	A_33_P3376745	3,913	up		
188	A_33_P3390177	3,908	up	FLJ34208	Homo sapiens hypothetical LOC401106 (FLJ34208), non-coding RNA [NR_033929]
189	A_23_P131215	3,898	up	CRYGD	Homo sapiens crystallin, gamma D (CRYGD), mRNA [NM_006891]
190	A_23_P4160	3,897	up	NBR2	Homo sapiens neighbor of BRCA1 gene 2 (non-protein coding) (NBR2), non-coding RNA [NR_003108]
191	A_32_P211418	3,892	up	CXorf41	Homo sapiens chromosome X open reading frame 41 (CXorf41), transcript variant 2, mRNA [NM_173494]
192	A_33_P3655646	3,889	up	LOC100130354	Homo sapiens hypothetical protein LOC100130354, mRNA (cDNA clone MGC:97363 IMAGE:7262624), complete cds, [BC069735]
193	A_23_P80242	3,888	up	SEZ6L	Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), transcript variant 1, mRNA [NM_021115]
194	A_33_P3263518	3,887	up		chromosome 12 open reading frame 63 [Source:HGNC Symbol;Acc:24777] [ENST00000298953]
195	A_23_P28186	3,861	up	SRD5A2	Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2) (SRD5A2), mRNA [NM_000348]
196	A_33_P3313125	3,855	up		
197	A_23_P319027	3,851	up	HECW1	Homo sapiens HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1 (HECW1), mRNA [NM_015052]
198	A_23_P29153	3,851	up	RTDR1	Homo sapiens rhabdoid tumor deletion region gene 1 (RTDR1), mRNA [NM_014433]
199	A_32_P60635	3,834	up	LOC643037	Homo sapiens hypothetical protein LOC643037 (LOC643037), mRNA [NM_001190462]
200	A_32_P61495	3,834	up	FHAD1	Homo sapiens forkhead-associated (FHA) phosphopeptide binding domain 1 (FHAD1), mRNA [NM_052929]
201	A_23_P402331	3,826	up	WFDC5	Homo sapiens WAP four-disulfide core domain 5 (WFDC5), mRNA [NM_145652]
202	A_33_P3306679	3,824	up	PLEKHG7	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 7 (PLEKHG7), mRNA [NM_001004330]
203	A_33_P3348220	3,820	up	ENGASE	Homo sapiens endo-beta-N-acetylglucosaminidase (ENGASE), mRNA [NM_001042573]
204	A_33_P3275630	3,818	up	LOC100131820	Homo sapiens cDNA FLJ43625 fis, clone SPLEN2024127, [AK125613]
205	A_23_P64808	3,804	up	HOXC13	Homo sapiens homeobox C13 (HOXC13), mRNA [NM_017410]
206	A_32_P203528	3,801	up	SYCE2	Homo sapiens synaptonemal complex central element protein 2 (SYCE2), mRNA [NM_001105578]
207	A_33_P3242829	3,792	up	PKN2	protein kinase N2 [Source:HGNC Symbol;Acc:9406] [ENST00000316005]
208	A_33_P3341836	3,784	up	ZNF780B	Homo sapiens zinc finger protein 780B (ZNF780B), mRNA [NM_001005851]
209	A_24_P34534	3,778	up	PARD3B	Homo sapiens par-3 partitioning defective 3 homolog B (C, elegans) (PARD3B), mRNA [NM_152526]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
210	A_23_P422732	3,778	up	WDR63	Homo sapiens WD repeat domain 63 (WDR63), mRNA [NM_145172]
211	A_23_P421054	3,776	up	C6orf165	Homo sapiens chromosome 6 open reading frame 165 (C6orf165), mRNA [NM_001031743]
212	A_33_P3387164	3,773	up	TCP11	Homo sapiens t-complex 11 homolog (mouse) (TCP11), transcript variant 2, mRNA [NM_018679]
213	A_33_P3241884	3,773	up	SDC3	Homo sapiens syndecan 3 (SDC3), mRNA [NM_014654]
214	A_33_P3293265	3,771	up		
215	A_33_P3408514	3,765	up	SCNN1D	Homo sapiens sodium channel, nonvoltage-gated 1, delta (SCNN1D), transcript variant 1, mRNA [NM_001130413]
216	A_33_P3345534	3,754	up	KRT14	Homo sapiens keratin 14 (KRT14), mRNA [NM_000526]
217	A_33_P3328726	3,750	up	CCDC33	Homo sapiens coiled-coil domain containing 33 (CCDC33), transcript variant 2, mRNA [NM_182791]
218	A_33_P3319126	3,737	up	CR1L	Homo sapiens complement component (3b/4b) receptor 1-like (CR1L), mRNA [NM_175710]
219	A_33_P3276250	3,735	up	TMEM191C	Homo sapiens cDNA, FLJ98745, [AK308704]
220	A_33_P3416787	3,734	up		
221	A_33_P3318444	3,722	up	RNF222	Homo sapiens ring finger protein 222 (RNF222), mRNA [NM_001146684]
222	A_24_P918175	3,721	up	LOC653581	Homo sapiens TANK-binding kinase 1, mRNA (cDNA clone IMAGE:3938647), partial cds, [BC009864]
223	A_33_P3385671	3,718	up		
224	A_33_P3389898	3,713	up	OR4D11	Homo sapiens olfactory receptor, family 4, subfamily D, member 11 (OR4D11), mRNA [NM_001004706]
225	A_33_P3340189	3,708	up		
226	A_33_P3214076	3,702	up		
227	A_23_P89101	3,702	up	Sep 12	Homo sapiens septin 12 (SEPT12), transcript variant 2, mRNA [NM_144605]
228	A_23_P92860	3,698	up	CCNO	Homo sapiens cyclin O (CCNO), mRNA [NM_021147]
229	A_33_P3315149	3,696	up	C15orf34	Homo sapiens chromosome 15 open reading frame 34 (C15orf34), non-coding RNA [NR_027262]
230	A_23_P75008	3,696	up	GAD2	Homo sapiens glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa) (GAD2), transcript variant 1, mRNA [NM_000818]
231	A_23_P64525	3,694	up	RAG2	Homo sapiens recombination activating gene 2 (RAG2), transcript variant 1, mRNA [NM_000536]
232	A_23_P67569	3,691	up	LPPR3	Homo sapiens lipid phosphate phosphatase-related protein type 3 (LPPR3), mRNA [NM_024888]
233	A_33_P3419239	3,691	up	DNAI2	Homo sapiens dynein, axonemal, intermediate chain 2 (DNAI2), transcript variant 1, mRNA [NM_023036]
234	A_33_P3320832	3,684	up	NMS	Homo sapiens neuromedin S (NMS), mRNA [NM_001011717]
235	A_23_P362770	3,676	up	CCDC36	Homo sapiens coiled-coil domain containing 36 (CCDC36), transcript variant 1, mRNA [NM_178173]
236	A_23_P10385	3,672	up	DTL	Homo sapiens denticleless homolog (Drosophila) (DTL), mRNA [NM_016448]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
237	A_23_P101048	3,661	up	KRTAP3-2	Homo sapiens keratin associated protein 3-2 (KRTAP3-2), mRNA [NM_031959]
238	A_33_P3282374	3,647	up	TIAM2	T-cell lymphoma invasion and metastasis 2 [Source:HGNC Symbol;Acc:11806] [ENST00000535064]
239	A_23_P56578	3,646	up	VIT	Homo sapiens vitrin (VIT), transcript variant 1, mRNA [NM_053276]
240	A_33_P3311791	3,643	up	ZNF749	Homo sapiens zinc finger protein 749 (ZNF749), mRNA [NM_001023561]
241	A_33_P3334738	3,637	up		
242	A_24_P16143	3,636	up	CDHR4	Homo sapiens cadherin-related family member 4 (CDHR4), mRNA [NM_001007540]
243	A_24_P820037	3,634	up	SLC6A17	Homo sapiens solute carrier family 6, member 17 (SLC6A17), mRNA [NM_001010898]
244	A_33_P3313456	3,627	up	CXorf30	Homo sapiens chromosome X open reading frame 30 (CXorf30), mRNA [NM_001098843]
245	A_23_P348636	3,626	up	FOXJ1	Homo sapiens forkhead box J1 (FOXJ1), mRNA [NM_001454]
246	A_33_P3403708	3,623	up		
247	A_33_P3354451	3,622	up	TRIM31	Homo sapiens tripartite motif containing 31 (TRIM31), mRNA [NM_007028]
248	A_33_P3245168	3,621	up	FAM71F2	Homo sapiens family with sequence similarity 71, member F2 (FAM71F2), transcript variant 2, mRNA [NM_001128926]
249	A_33_P3217649	3,615	up	C9orf116	Homo sapiens chromosome 9 open reading frame 116 (C9orf116), transcript variant 1, mRNA [NM_001048265]
250	A_33_P3278826	3,601	up	LTK	leukocyte receptor tyrosine kinase [Source:HGNC Symbol;Acc:6721] [ENST00000360087]
251	A_33_P3313825	3,595	up	TGFBR2	transforming growth factor, beta receptor II (70/80kDa) [Source:HGNC Symbol;Acc:11773] [ENST00000383765]
252	A_23_P86710	3,594	up	FRMPD2	Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), transcript variant 3, mRNA [NM_001018071]
253	A_23_P326157	3,591	up	GAL3ST2	Homo sapiens galactose-3-O-sulfotransferase 2 (GAL3ST2), mRNA [NM_022134]
254	A_24_P66337	3,590	up	LCLAT1	lysocardiolipin acyltransferase 1 [Source:HGNC Symbol;Acc:26756] [ENST00000319406]
255	A_33_P3303339	3,587	up		
256	A_33_P3216200	3,581	up		
257	A_33_P3407751	3,579	up		Homo sapiens cDNA FLJ44041 fis, clone TESTI4029370, [AK126029]
258	A_32_P206899	3,570	up	DNAH2	Homo sapiens dynein, axonemal, heavy chain 2 (DNAH2), mRNA [NM_020877]
259	A_24_P24053	3,567	up		immunoglobulin heavy variable 3-66 [Source:HGNC Symbol;Acc:5619] [ENST00000390632]
260	A_33_P3383292	3,564	up	LOC100129620	Homo sapiens hypothetical LOC100129620 (LOC100129620), non-coding RNA [NR_033940]
261	A_33_P3303890	3,563	up	OR52A4	olfactory receptor, family 52, subfamily A, member 4 [Source:HGNC Symbol;Acc:19579] [ENST00000380369]
262	A_33_P3422124	3,562	up	IL22RA2	Homo sapiens interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 3, mRNA [NM_181310]
263	A_33_P3327673	3,561	up	COBL	Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA [NM_015198]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
264	A_33_P3272773	3,550	up	ZNF217	Homo sapiens zinc finger protein 217 (ZNF217), mRNA [NM_006526]
265	A_23_P409449	3,548	up	TAL2	Homo sapiens T-cell acute lymphocytic leukemia 2 (TAL2), mRNA [NM_005421]
266	A_33_P3281250	3,544	up		T cell receptor beta variable 7-1 (non-functional) [Source:HGNC Symbol;Acc:12235] [ENST00000390354]
267	A_23_P321160	3,537	up	ZNF594	Homo sapiens zinc finger protein 594 (ZNF594), mRNA [NM_032530]
268	A_23_P212608	3,536	up	CLSTN2	Homo sapiens calsyntenin 2 (CLSTN2), mRNA [NM_022131]
269	A_33_P3260862	3,536	up		ALU7_HUMAN (P39194) Alu subfamily SQ sequence contamination warning entry, partial (14%) [THC2503512]
270	A_33_P3346483	3,530	up	SYNPO2L	synaptopodin 2-like [Source:HGNC Symbol;Acc:23532] [ENST00000394810]
271	A_33_P3216746	3,527	up	LPHN3	Homo sapiens latrophilin 3 (LPHN3), mRNA [NM_015236]
272	A_33_P3687198	3,524	up	LOC283454	Homo sapiens cDNA FLJ37411 fis, clone BRAMY2028682, [AK094730]
273	A_32_P56397	3,519	up	LOC731789	Homo sapiens hypothetical LOC731789 (LOC731789), non-coding RNA [NR_026794]
274	A_32_P100830	3,515	up	KIF19	Homo sapiens kinesin family member 19 (KIF19), mRNA [NM_153209]
275	A_33_P3749100	3,513	up	LOC285045	Homo sapiens hypothetical LOC285045 (LOC285045), transcript variant 1, non-coding RNA [NR_027098]
276	A_33_P3323019	3,512	up	LOC729856	PREDICTED: Homo sapiens elongation factor 1-alpha-like (LOC729856), mRNA [XM_001130188]
277	A_23_P68978	3,509	up	EFCAB6	Homo sapiens EF-hand calcium binding domain 6 (EFCAB6), transcript variant 1, mRNA [NM_022785]
278	A_23_P413862	3,506	up	DCDC5	Homo sapiens doublecortin domain containing 5 (DCDC5), mRNA [NM_020869]
279	A_24_P150791	3,498	up	JPH3	Homo sapiens junctophilin 3 (JPH3), mRNA [NM_020655]
280	A_33_P3420259	3,496	up	RN28S1	Homo sapiens RNA, 28S ribosomal 1 (RN28S1), ribosomal RNA [NR_003287]
281	A_33_P3360456	3,494	up	ZNF154	Homo sapiens zinc finger protein 154 (ZNF154), mRNA [NM_001085384]
282	A_33_P3313755	3,493	up	PRAMEF22	Homo sapiens PRAME family member 22 (PRAMEF22), mRNA [NM_001100631]
283	A_33_P3338047	3,484	up	PNPLA7	Homo sapiens patatin-like phospholipase domain containing 7 (PNPLA7), transcript variant 1, mRNA [NM_001098537]
284	A_33_P3337252	3,481	up	WWC2	WW and C2 domain containing 2 [Source:HGNC Symbol;Acc:24148] [ENST00000378925]
285	A_23_P130906	3,481	up	TEX101	Homo sapiens testis expressed 101 (TEX101), transcript variant 1, mRNA [NM_031451]
286	A_33_P3357303	3,474	up	OR5W2	Homo sapiens olfactory receptor, family 5, subfamily W, member 2 (OR5W2), mRNA [NM_001001960]
287	A_33_P3384427	3,473	up		
288	A_23_P501193	3,472	up	KCNJ16	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), transcript variant 2, mRNA [NM_170741]
289	A_33_P3214334	3,464	up	LY6G6F	Homo sapiens lymphocyte antigen 6 complex, locus G6F (LY6G6F), mRNA [NM_001003693]
290	A_23_P252276	3,463	up	ARHGEF38	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 38 (ARHGEF38), transcript variant 2, mRNA [NM_017700]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
291	A_33_P3291772	3,463	up		
292	A_33_P3315169	3,453	up		GB
293	A_33_P3464438	3,449	up		non-protein coding RNA 221 [Source:HGNC Symbol;Acc:20169] [ENST00000433371]
294	A_33_P3397198	3,449	up		DB013410 TESOP2 Homo sapiens cDNA clone TESOP2001961 5', mRNA sequence [DB013410]
295	A_23_P386442	3,448	up	KIAA0087	Homo sapiens KIAA0087 (KIAA0087), non-coding RNA [NR_022006]
296	A_23_P395404	3,447	up	FGF20	Homo sapiens fibroblast growth factor 20 (FGF20), mRNA [NM_019851]
297	A_33_P3336632	3,440	up	RN28S1	Homo sapiens RNA, 28S ribosomal 1 (RN28S1), ribosomal RNA [NR_003287]
298	A_33_P3379356	3,437	up	ESR1	Homo sapiens estrogen receptor 1 (ESR1), transcript variant 4, mRNA [NM_001122742]
299	A_32_P144342	3,437	up	PARP4	Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), mRNA [NM_006437]
300	A_33_P3857239	3,428	up	KRT42P	Homo sapiens keratin 42 pseudogene (KRT42P), non-coding RNA [NR_033415]
301	A_33_P3275000	3,426	up	ZBTB40	Homo sapiens zinc finger and BTB domain containing 40 (ZBTB40), transcript variant 1, mRNA [NM_001083621]
302	A_33_P3410821	3,424	up		
303	A_23_P57248	3,424	up	C20orf173	Homo sapiens chromosome 20 open reading frame 173 (C20orf173), transcript variant 1, mRNA [NM_001145350]
304	A_23_P47904	3,422	up	CCDC65	Homo sapiens coiled-coil domain containing 65 (CCDC65), mRNA [NM_033124]
305	A_23_P361544	3,420	up	CES4A	Homo sapiens carboxylesterase 4A (CES4A), transcript variant 1, mRNA [NM_173815]
306	A_24_P887857	3,419	up		
307	A_33_P3394366	3,417	up		C-type lectin domain family 19, member A [Source:HGNC Symbol;Acc:34522] [ENST00000468219]
308	A_23_P69012	3,417	up	CCR8	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8), mRNA [NM_005201]
309	A_33_P3304691	3,414	up	KRTAP5-1	Homo sapiens keratin associated protein 5-1 (KRTAP5-1), mRNA [NM_001005922]
310	A_23_P374919	3,413	up	LRRC71	Homo sapiens leucine rich repeat containing 71 (LRRC71), mRNA [NM_144702]
311	A_33_P3269503	3,405	up		Homo sapiens cDNA FLJ60029 complete cds, highly similar to Keratin, type II cuticular Hb3, [AK300121]
312	A_23_P362736	3,396	up	RSPH10B	Homo sapiens radial spoke head 10 homolog B (Chlamydomonas) (RSPH10B), mRNA [NM_173565]
313	A_33_P3285799	3,395	up	AKD1	adenylate kinase domain containing 1 [Source:HGNC Symbol;Acc:33814] [ENST00000341338]
314	A_33_P3325285	3,387	up		BC034563 ACBD3 protein {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (17%) [THC2682346]
315	A_24_P211797	3,377	up	ICA1L	Homo sapiens islet cell autoantigen 1,69kDa-like (ICA1L), transcript variant 2, mRNA [NM_178231]
316	A_33_P3240158	3,376	up		
317	A_33_P3362409	3,368	up	LOC100499484	Homo sapiens SUGT1-1300002K09Rik pseudogene (LOC100499484), non-coding RNA [NR_036526]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
318	A_24_P388786	3,367	up	DNAH5	Homo sapiens dynein, axonemal, heavy chain 5 (DNAH5), mRNA [NM_001369]
319	A_33_P3338484	3,363	up		DKFZp686M06185_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686M06185 5', mRNA sequence [BX476374]
320	A_23_P52480	3,363	up	CYP2C18	Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 18 (CYP2C18), transcript variant 1, mRNA [NM_000772]
321	A_24_P77947	3,350	up	CCDC132	Homo sapiens coiled-coil domain containing 132 (CCDC132), transcript variant 2, mRNA [NM_024553]
322	A_23_P379789	3,350	up	ST8SIA5	Homo sapiens ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 (ST8SIA5), mRNA [NM_013305]
323	A_33_P3214988	3,344	up	EFCAB1	Homo sapiens EF-hand calcium binding domain 1 (EFCAB1), transcript variant 2, mRNA [NM_001142857]
324	A_33_P3225760	3,344	up	PCDH18	Homo sapiens protocadherin 18 (PCDH18), mRNA [NM_019035]
325	A_23_P68910	3,343	up	SSTR3	Homo sapiens somatostatin receptor 3 (SSTR3), mRNA [NM_001051]
326	A_23_P126499	3,334	up	RSG1	Homo sapiens REM2 and RAB-like small GTPase 1 (RSG1), mRNA [NM_030907]
327	A_33_P3238533	3,329	up	C18orf34	Homo sapiens chromosome 18 open reading frame 34 (C18orf34), transcript variant 1, mRNA [NM_001105528]
328	A_33_P3302300	3,328	up	LOC100128333	Homo sapiens cDNA FLJ45779 fis, clone NETRP2005282, [AK127681]
329	A_23_P97826	3,323	up	TECTB	Homo sapiens tectorin beta (TECTB), mRNA [NM_058222]
330	A_33_P3277361	3,322	up	OTX1	Homo sapiens orthodenticle homeobox 1 (OTX1), transcript variant 2, mRNA [NM_001199770]
331	A_24_P162173	3,322	up	ANK3	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 2, mRNA [NM_001149]
332	A_33_P3329448	3,321	up		PREDICTED: Homo sapiens hypothetical protein LOC730198 (LOC730198), mRNA [XM_001132891]
333	A_33_P3364062	3,319	up	FLJ31356	PREDICTED: Homo sapiens hypothetical protein FLJ31356 (FLJ31356), partial miscRNA [XR_109966]
334	A_24_P315444	3,318	up		
335	A_23_P148568	3,317	up	NXF2	Homo sapiens nuclear RNA export factor 2 (NXF2), mRNA [NM_022053]
336	A_33_P3400309	3,314	up	C6orf103	chromosome 6 open reading frame 103 [Source:HGNC Symbol;Acc:21212] [ENST00000326929]
337	A_33_P3585924	3,311	up	LOC339529	Homo sapiens hypothetical LOC339529 (LOC339529), non-coding RNA [NR_033883]
338	A_24_P882732	3,310	up		keratin 17 pseudogene 1 [Source:HGNC Symbol;Acc:6428] [ENST00000399211]
339	A_33_P3350259	3,307	up	FAM129C	Homo sapiens family with sequence similarity 129, member C (FAM129C), transcript variant 2, mRNA [NM_001098524]
340	A_33_P3412143	3,305	up	RASSF10	Homo sapiens Ras association (RalGDS/AF-6) domain family (N-terminal) member 10 (RASSF10), mRNA [NM_001080521]
341	A_33_P3374215	3,304	up		
342	A_33_P3397593	3,295	up		
343	A_33_P3424108	3,292	up		
344	A_33_P3313855	3,292	up	LOC100127951	Homo sapiens clone DNA142958 ISPF6484 (UNQ6484) mRNA, complete cds, [AY358233]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
345	A_23_P133338	3,289	up	CDHR2	Homo sapiens cadherin-related family member 2 (CDHR2), transcript variant 2, mRNA [NM_017675]
346	A_33_P3344297	3,288	up		
347	A_23_P5211	3,286	up	MUC16	Homo sapiens mucin 16, cell surface associated (MUC16), mRNA [NM_024690]
348	A_23_P415820	3,284	up	EXOC6B	Homo sapiens mRNA for KIAA0919 protein, partial cds, [AB023136]
349	A_32_P199901	3,283	up	RIPPLY1	Homo sapiens ripply1 homolog (zebrafish) (RIPPLY1), transcript variant 1, mRNA [NM_138382]
350	A_33_P3381191	3,282	up	FOXRED2	Homo sapiens FAD-dependent oxidoreductase domain containing 2 (FOXRED2), transcript variant 1, mRNA [NM_024955]
351	A_33_P3394993	3,278	up	PREX2	Homo sapiens phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2 (PREX2), transcript variant 2, mRNA [NM_025170]
352	A_23_P10542	3,278	up	HTRA3	Homo sapiens HtrA serine peptidase 3 (HTRA3), mRNA [NM_053044]
353	A_33_P3285629	3,277	up	DNAI2	Homo sapiens dynein, axonemal, intermediate chain 2 (DNAI2), transcript variant 1, mRNA [NM_023036]
354	A_23_P154784	3,271	up	C20orf114	Homo sapiens chromosome 20 open reading frame 114 (C20orf114), mRNA [NM_033197]
355	A_33_P3390122	3,270	up	GIPC2	Homo sapiens GIPC PDZ domain containing family, member 2 (GIPC2), mRNA [NM_017655]
356	A_24_P303199	3,270	up	ARL15	Homo sapiens ADP-ribosylation factor-like 15 (ARL15), mRNA [NM_019087]
357	A_32_P141418	3,268	up	ARMC4	Homo sapiens armadillo repeat containing 4 (ARMC4), mRNA [NM_018076]
358	A_33_P3357232	3,258	up		
359	A_33_P3225022	3,254	up	FTCD	Homo sapiens formiminotransferase cyclodeaminase (FTCD), transcript variant A, mRNA [NM_206965]
360	A_33_P3398074	3,249	up	LOC100133319	Homo sapiens PRO1804 mRNA, complete cds, [AF132201]
361	A_23_P163099	3,249	up	POLE2	Homo sapiens polymerase (DNA directed), epsilon 2 (p59 subunit) (POLE2), transcript variant 1, mRNA [NM_002692]
362	A_33_P3258244	3,248	up	PCDH15	Homo sapiens protocadherin-related 15 (PCDH15), transcript variant K, mRNA [NM_001142771]
363	A_33_P3369716	3,244	up		Q9VKG5_DROME (Q9VKG5) CG14930-PA (AT28291p), partial (5%) [THC2679405]
364	A_33_P3316953	3,241	up	RBFOX3	Homo sapiens RNA binding protein, fox-1 homolog (C, elegans) 3 (RBFOX3), mRNA [NM_001082575]
365	A_24_P66605	3,241	up	SLITRK2	Homo sapiens SLIT and NTRK-like family, member 2 (SLITRK2), transcript variant 1, mRNA [NM_032539]
366	A_23_P64161	3,240	up	ANGPTL5	Homo sapiens angiopoietin-like 5 (ANGPTL5), mRNA [NM_178127]
367	A_33_P3825317	3,234	up	LOC646851	Homo sapiens hypothetical LOC646851 (LOC646851), mRNA [NM_001013647]
368	A_33_P3366850	3,232	up		Homo sapiens mRNA for T cell receptor alpha variable 12, partial cds, clone: un 85, [AB306031]
369	A_23_P49546	3,231	up	GRIN2C	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2C (GRIN2C), mRNA [NM_000835]
370	A_24_P100650	3,226	up	C9orf11	Homo sapiens chromosome 9 open reading frame 11 (C9orf11), transcript variant 1, mRNA [NM_020641]
371	A_23_P396724	3,225	up	LRRC43	Homo sapiens leucine rich repeat containing 43 (LRRC43), transcript variant 2, mRNA [NM_152759]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
372	A_23_P300090	3,223	up	SLC10A7	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 7 (SLC10A7), transcript variant 3, mRNA [NM_032128]
373	A_33_P3239143	3,222	up	ZNF497	Homo sapiens zinc finger protein 497 (ZNF497), mRNA [NM_198458]
374	A_33_P3417328	3,221	up	SHROOM3	shroom family member 3 [Source:HGNC Symbol;Acc:30422] [ENST00000380735]
375	A_33_P3220352	3,220	up	CNPY1	Homo sapiens canopy 1 homolog (zebrafish) (CNPY1), mRNA [NM_001103176]
376	A_33_P3360249	3,214	up	HCRTR1	Homo sapiens hypocretin (orexin) receptor 1 (HCRTR1), mRNA [NM_001525]
377	A_23_P39056	3,209	up	KLK7	Homo sapiens kallikrein-related peptidase 7 (KLK7), transcript variant 1, mRNA [NM_005046]
378	A_33_P3242878	3,202	up	EFCAB6	Homo sapiens EF-hand calcium binding domain 6 (EFCAB6), transcript variant 1, mRNA [NM_022785]
379	A_33_P3227047	3,201	up	LOC646934	PREDICTED: Homo sapiens putative golgin subfamily A member 6D-like (LOC646934), mRNA [XM_003120816]
380	A_33_P3302881	3,200	up	KLHL31	Homo sapiens kelch-like 31 (Drosophila) (KLHL31), mRNA [NM_001003760]
381	A_32_P449380	3,192	up	WDR38	Homo sapiens WD repeat domain 38 (WDR38), mRNA [NM_001045476]
382	A_33_P3324415	3,192	up	LOC642414	PREDICTED: Homo sapiens putative tripartite motif-containing protein 64B-like (LOC642414), mRNA [XM_003119181]
383	A_33_P3291154	3,191	up	ZBTB20	Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), transcript variant 3, mRNA [NM_001164343]
384	A_33_P3300027	3,190	up		
385	A_33_P3317327	3,185	up	TRPM8	transient receptor potential cation channel, subfamily M, member 8 [Source:HGNC Symbol;Acc:17961] [ENST00000355722]
386	A_23_P23996	3,184	up	MAT1A	Homo sapiens methionine adenosyltransferase I, alpha (MAT1A), mRNA [NM_000429]
387	A_33_P3333667	3,184	up	XRRA1	Homo sapiens X-ray radiation resistance associated 1 (XRRA1), mRNA [NM_182969]
388	A_33_P3239989	3,183	up		
389	A_33_P3321417	3,182	up	DMAP1	Homo sapiens DNA methyltransferase 1 associated protein 1 (DMAP1), transcript variant 1, mRNA [NM_019100]
390	A_33_P3236436	3,178	up	C4orf51	Homo sapiens chromosome 4 open reading frame 51 (C4orf51), mRNA [NM_001080531]
391	A_33_P3398597	3,176	up	EPS8L1	Homo sapiens EPS8-like 1 (EPS8L1), transcript variant 1, mRNA [NM_133180]
392	A_33_P3221403	3,176	up	LOC646743	Homo sapiens clone TESTIS-608 mRNA sequence, [AY726562]
393	A_33_P3333272	3,174	up	TMEM235	Homo sapiens transmembrane protein 235 (TMEM235), transcript variant 1, mRNA [NM_001204210]
394	A_33_P3247165	3,169	up	CT62	Homo sapiens cancer/testis antigen 62 (CT62), mRNA [NM_001102658]
395	A_23_P131683	3,167	up	MAPRE3	Homo sapiens microtubule-associated protein, RP/EB family, member 3 (MAPRE3), mRNA [NM_012326]
396	A_33_P3346688	3,163	up	HSPA8	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:5241] [ENST00000527983]
397	A_33_P3240234	3,162	up		PREDICTED: Homo sapiens similar to hCG1644435 (LOC100131818), mRNA [XM_001725646]
398	A_23_P70643	3,162	up	C6orf103	Homo sapiens chromosome 6 open reading frame 103 (C6orf103), mRNA [NM_024694]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
399	A_33_P3296807	3,155	up	HDAC8	Homo sapiens histone deacetylase 8 (HDAC8), transcript variant 3, mRNA [NM_001166419]
400	A_33_P3226460	3,152	up		
401	A_33_P3304506	3,149	up		
402	A_33_P3231700	3,148	up	ZNF677	zinc finger protein 677 [Source:HGNC Symbol;Acc:28730] [ENST00000333952]
403	A_24_P409985	3,147	up	TMEM44	Homo sapiens transmembrane protein 44 (TMEM44), transcript variant 2, mRNA [NM_001011655]
404	A_33_P3284045	3,142	up	NEK10	Homo sapiens NIMA (never in mitosis gene a)- related kinase 10 (NEK10), mRNA [NM_199347]
405	A_33_P3359027	3,141	up	CCDC42B	Homo sapiens coiled-coil domain containing 42B (CCDC42B), mRNA [NM_001144872]
406	A_33_P3260974	3,140	up		DA734158 NT2RP2 Homo sapiens cDNA clone NT2RP2004573 5', mRNA sequence [DA734158]
407	A_24_P3415	3,137	up	PPP2R2C	Homo sapiens protein phosphatase 2, regulatory subunit B, gamma (PPP2R2C), transcript variant 2, mRNA [NM_181876]
408	A_23_P7048	3,136	up	C4orf6	Homo sapiens chromosome 4 open reading frame 6 (C4orf6), mRNA [NM_005750]
409	A_23_P96158	3,135	up	KRT17	Homo sapiens keratin 17 (KRT17), mRNA [NM_000422]
410	A_23_P320829	3,134	up	CEP128	Homo sapiens centrosomal protein 128kDa (CEP128), mRNA [NM_152446]
411	A_33_P3222867	3,134	up	THBS3	Homo sapiens mRNA; cDNA DKFZp686J1738 (from clone DKFZp686J1738), [CR933610]
412	A_33_P3293466	3,123	up		
413	A_23_P132004	3,120	up	C20orf71	Homo sapiens chromosome 20 open reading frame 71 (C20orf71), transcript variant 1, mRNA [NM_178466]
414	A_33_P3296721	3,117	up		
415	A_33_P3262475	3,115	up	SERP2	stress-associated endoplasmic reticulum protein family member 2 [Source:HGNC Symbol;Acc:20607] [ENST00000474333]
416	A_33_P3251144	3,115	up	CDCA7L	Homo sapiens cell division cycle associated 7-like (CDCA7L), transcript variant 2, mRNA [NM_001127370]
417	A_32_P76627	3,109	up		full-length cDNA clone CS0DI013YN06 of Placenta Cot 25-normalized of Homo sapiens (human), [CR597597]
418	A_24_P305050	3,108	up	CD300LG	Homo sapiens CD300 molecule-like family member g (CD300LG), transcript variant 1, mRNA [NM_145273]
419	A_32_P221907	3,106	up	C6orf10	Homo sapiens chromosome 6 open reading frame 10 (C6orf10), mRNA [NM_006781]
420	A_33_P3383174	3,102	up	LOC644366	PREDICTED: Homo sapiens hypothetical protein LOC644366 (LOC644366), mRNA [XM_003120886]
421	A_33_P3385436	3,101	up	PLAC8L1	Homo sapiens PLAC8-like 1 (PLAC8L1), mRNA [NM_001029869]
422	A_23_P363275	3,098	up	WDR66	Homo sapiens WD repeat domain 66 (WDR66), transcript variant 1, mRNA [NM_144668]
423	A_24_P912048	3,097	up	MGC50722	Homo sapiens hypothetical MGC50722 (MGC50722), mRNA [NM_203348]
424	A_23_P419696	3,097	up	LYPD1	Homo sapiens LY6/PLAUR domain containing 1 (LYPD1), transcript variant 1, mRNA [NM_144586]
425	A_23_P43846	3,096	up	FABP6	Homo sapiens fatty acid binding protein 6, ileal (FABP6), transcript variant 1, mRNA [NM_001040442]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
426	A_33_P3263851	3,095	up		PREDICTED: Homo sapiens FLJ46020 protein (FLJ46020), miscRNA [XR_109667]
427	A_23_P75867	3,095	up	OR10A4	Homo sapiens olfactory receptor, family 10, subfamily A, member 4 (OR10A4), mRNA [NM_207186]
428	A_23_P110319	3,091	up	CWH43	Homo sapiens cell wall biogenesis 43 C-terminal homolog (S, cerevisiae) (CWH43), mRNA [NM_025087]
429	A_33_P3660204	3,089	up	LOC340073	Homo sapiens hypothetical LOC340073 (LOC340073), non-coding RNA [NR_037895]
430	A_24_P921683	3,086	up	FOXP2	Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA [NM_014491]
431	A_33_P3336262	3,086	up	KIAA1751	chromosome 1 open reading frame 222 [Source:HGNC Symbol;Acc:27917] [ENST00000412120]
432	A_23_P388871	3,084	up	HIST4H4	Homo sapiens histone cluster 4, H4 (HIST4H4), mRNA [NM_175054]
433	A_33_P3391521	3,083	up	ERO1LB	ERO1-like beta (S, cerevisiae) [Source:HGNC Symbol;Acc:14355] [ENST00000366589]
434	A_23_P18362	3,082	up	SLITRK3	Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), mRNA [NM_014926]
435	A_33_P3259625	3,081	up	TTC34	Homo sapiens tetratricopeptide repeat domain 34 (TTC34), mRNA [NM_001242672]
436	A_23_P123096	3,079	up	GNGT1	Homo sapiens guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1 (GNGT1), mRNA [NM_021955]
437	A_33_P3369854	3,079	up	DNAJB13	Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 13 (DNAJB13), mRNA [NM_153614]
438	A_23_P148327	3,077	up	CACNA1F	Homo sapiens calcium channel, voltage-dependent, L type, alpha 1F subunit (CACNA1F), mRNA [NM_005183]
439	A_33_P3268161	3,074	up		
440	A_32_P126229	3,073	up	FLJ23152	Homo sapiens hypothetical protein LOC401236 (FLJ23152), mRNA [NM_001190766]
441	A_23_P139635	3,073	up	DAO	Homo sapiens D-amino-acid oxidase (DAO), mRNA [NM_001917]
442	A_33_P3303212	3,072	up	CCDC74B	Homo sapiens coiled-coil domain containing 74B (CCDC74B), mRNA [NM_207310]
443	A_33_P3225106	3,063	up	SLITRK2	SLIT and NTRK-like family, member 2 [Source:HGNC Symbol;Acc:13449] [ENST00000370490]
444	A_23_P94840	3,060	up	DYNLRB2	Homo sapiens dynein, light chain, roadblock-type 2 (DYNLRB2), mRNA [NM_130897]
445	A_33_P3284004	3,058	up	GNN	Homo sapiens Grp94 neighboring nucleotidase pseudogene (GNN), non-coding RNA [NR_027249]
446	A_23_P146294	3,056	up	EFCAB1	Homo sapiens EF-hand calcium binding domain 1 (EFCAB1), transcript variant 1, mRNA [NM_024593]
447	A_33_P3413114	3,050	up	ADAMTSL1	Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA [NM_052866]
448	A_32_P197524	3,048	up	EIF2A	Homo sapiens eukaryotic translation initiation factor 2A, 65kDa (EIF2A), mRNA [NM_032025]
449	A_33_P3238390	3,048	up	LOC389217	PREDICTED: Homo sapiens protein SET-like (LOC389217), mRNA [XM_001717714]
450	A_33_P3233995	3,047	up	BAALC	brain and acute leukemia, cytoplasmic [Source:HGNC Symbol;Acc:14333] [ENST00000330955]
451	A_33_P3333327	3,047	up		
452	A_33_P3333600	3,044	up		cDNA FLJ42903 fis, clone BRHIP3013765 [Source:UniProtKB/TrEMBL;Acc:Q6ZV80] [ENST00000403980]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
453	A_33_P3399218	3,044	up		HUMRPS7A ribosomal protein {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (65%) [THC2633659]
454	A_33_P3409422	3,037	up		DB047837 TESTI2 Homo sapiens cDNA clone TESTI2036726 5', mRNA sequence [DB047837]
455	A_23_P307274	3,036	up	OR2H2	Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), mRNA [NM_007160]
456	A_23_P364324	3,035	up	ABCA13	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 13 (ABCA13), mRNA [NM_152701]
457	A_33_P3227686	3,035	up	FLJ43860	Homo sapiens FLJ43860 protein (FLJ43860), mRNA [NM_207414]
458	A_33_P3240687	3,035	up	LOC100287326	PREDICTED: Homo sapiens hypothetical protein LOC100287326 (LOC100287326), mRNA [XM_002343311]
459	A_33_P3240263	3,034	up	POMP	Homo sapiens proteasome maturation protein (POMP), mRNA [NM_015932]
460	A_33_P3279861	3,034	up		Homo sapiens clone 1120 immunoglobulin lambda light chain variable region mRNA, partial cds, [AF194718]
461	A_32_P34844	3,033	up	ADAMTS18	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 18 (ADAMTS18), mRNA [NM_199355]
462	A_33_P3387716	3,033	up	DMGDH	dimethylglycine dehydrogenase [Source:HGNC Symbol;Acc:24475] [ENST00000380311]
463	A_33_P3378772	3,032	up	FAM98B	Homo sapiens family with sequence similarity 98, member B (FAM98B), transcript variant 2, mRNA [NM_001042429]
464	A_23_P384532	3,031	up	CCDC11	Homo sapiens coiled-coil domain containing 11 (CCDC11), mRNA [NM_145020]
465	A_23_P518	3,027	up	VTCN1	Homo sapiens V-set domain containing T cell activation inhibitor 1 (VTCN1), mRNA [NM_024626]
466	A_24_P336718	3,025	up	RABIF	Homo sapiens RAB interacting factor (RABIF), mRNA [NM_002871]
467	A_33_P3372840	3,024	up	CXCL12	Homo sapiens chemokine (C-X-C motif) ligand 12 (CXCL12), transcript variant 3, mRNA [NM_001033886]
468	A_24_P183994	3,023	up	RASEF	RAS and EF-hand domain containing [Source:HGNC Symbol;Acc:26464] [ENST00000340717]
469	A_33_P3527931	3,021	up	C19orf69	Homo sapiens chromosome 19 open reading frame 69 (C19orf69), mRNA [NM_001130514]
470	A_33_P3374205	3,018	up	MKI67	Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), transcript variant 1, mRNA [NM_002417]
471	A_33_P3300232	3,018	up	HYDIN	Homo sapiens hydrocephalus inducing homolog (mouse) (HYDIN), transcript variant 1, mRNA [NM_032821]
472	A_33_P3321025	3,016	up	PLXNA4	Homo sapiens plexin A4 (PLXNA4), transcript variant 1, mRNA [NM_020911]
473	A_33_P3342305	3,015	up	ABCA8	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA [NM_007168]
474	A_33_P3718274	3,015	up	LOC285629	DB296219 BNGH42 Homo sapiens cDNA clone BNGH42003641 3', mRNA sequence [DB296219]
475	A_33_P3419360	3,014	up	LOC731789	Homo sapiens hypothetical LOC731789 (LOC731789), non-coding RNA [NR_026794]
476	A_23_P216712	3,010	up	TRPM6	Homo sapiens transient receptor potential cation channel, subfamily M, member 6 (TRPM6), transcript variant a, mRNA [NM_017662]
477	A_33_P3692979	3,008	up	LOC283485	Homo sapiens cDNA FLJ36543 fis, clone TRACH2006194, [AK093862]
478	A_32_P478512	3,007	up	DKFZP434L187	Homo sapiens hypothetical LOC26082 (DKFZP434L187), non-coding RNA [NR_026771]
479	A_33_P3718679	3,005	up	LOC283731	Homo sapiens hypothetical protein LOC283731, mRNA (cDNA clone IMAGE:4826227), [BC050067]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
480	A_23_P29663	3,004	up	ZMYND10	Homo sapiens zinc finger, MYND-type containing 10 (ZMYND10), mRNA [NM_015896]
481	A_33_P3363445	2,998	up		PREDICTED: Homo sapiens hypothetical LOC100506014, transcript variant 1 (LOC100506014), partial miscRNA [XR_109907]
482	A_33_P3371904	2,994	up	ASTN2	Homo sapiens astrotactin 2 (ASTN2), transcript variant 4, mRNA [NM_198188]
483	A_33_P3408232	2,993	up	PBMUCL1	Homo sapiens panbronchiolitis related mucin-like 1 (PBMUCL1), mRNA [NM_001198815]
484	A_32_P46238	2,991	up	LOC339240	Homo sapiens keratin pseudogene (LOC339240), non-coding RNA [NR_001443]
485	A_23_P355980	2,982	up	P2RX6	purinergic receptor P2X, ligand-gated ion channel, 6 [Source:HGNC Symbol;Acc:8538] [ENST00000413302]
486	A_33_P3232363	2,980	up	PRO0611	Homo sapiens PRO0611 protein (PRO0611), non-coding RNA [NR_002762]
487	A_33_P3396766	2,980	up	LOC100131738	PREDICTED: Homo sapiens hypothetical LOC100131738 (LOC100131738), partial miscRNA [XR_108808]
488	A_33_P3274439	2,977	up		DA109127 BRACE3 Homo sapiens cDNA clone BRACE3025572 5', mRNA sequence [DA109127]
489	A_24_P417664	2,977	up	CC2D2B	coiled-coil and C2 domain containing 2B [Source:HGNC Symbol;Acc:31666] [ENST00000469549]
490	A_33_P3318092	2,976	up	PPP1R3A	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (PPP1R3A), mRNA [NM_002711]
491	A_33_P3312885	2,974	up	LOC284379	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 pseudogene (LOC284379), non-coding RNA [NR_002938]
492	A_32_P126733	2,966	up	NOL4	Homo sapiens nucleolar protein 4 (NOL4), transcript variant 1, mRNA [NM_003787]
493	A_33_P3382344	2,966	up		EST11357 human nasopharynx Homo sapiens cDNA, mRNA sequence [CD694834]
494	A_33_P3352995	2,955	up	IFITM5	Homo sapiens interferon induced transmembrane protein 5 (IFITM5), mRNA [NM_001025295]
495	A_23_P428366	2,954	up	HORMAD2	Homo sapiens HORMA domain containing 2 (HORMAD2), mRNA [NM_152510]
496	A_33_P3323136	2,949	up	ENKUR	Homo sapiens enkurin, TRPC channel interacting protein (ENKUR), mRNA [NM_145010]
497	A_33_P3787635	2,947	up	LOC440600	Homo sapiens hypothetical LOC440600 (LOC440600), non-coding RNA [NR_036595]
498	A_33_P3286958	2,946	up	B3GALT2	Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 (B3GALT2), mRNA [NM_003783]
499	A_23_P362148	2,943	up	DNER	Homo sapiens delta/notch-like EGF repeat containing (DNER), mRNA [NM_139072]
500	A_33_P3259938	2,939	up	LOC100130547	PREDICTED: Homo sapiens hypothetical LOC100130547 (LOC100130547), partial miscRNA [XR_113275]
501	A_32_P517715	2,936	up	RAD51B	Homo sapiens RAD51 homolog B (S, cerevisiae) (RAD51B), transcript variant 3, mRNA [NM_133509]
502	A_24_P307289	2,936	up	TMEM95	Homo sapiens transmembrane protein 95 (TMEM95), mRNA [NM_198154]
503	A_24_P419039	2,935	up	PCDH19	Homo sapiens protocadherin 19 (PCDH19), transcript variant 2, mRNA [NM_020766]
504	A_23_P328642	2,934	up	ALS2CR11	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11 (ALS2CR11), transcript variant 2, mRNA [NM_152525]
505	A_32_P216566	2,928	up	RIPPLY2	Homo sapiens ripply2 homolog (zebrafish) (RIPPLY2), mRNA [NM_001009994]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
506	A_33_P3262440	2,923	up	LOC100509701	PREDICTED: Homo sapiens Golgin subfamily A member 6-like protein 2-like (LOC100509701), mRNA [XM_003119601]
507	A_33_P3288125	2,922	up	LOC284395	Homo sapiens hypothetical LOC284395 (LOC284395), non-coding RNA [NR_040029]
508	A_23_P308058	2,922	up	TUSC5	Homo sapiens tumor suppressor candidate 5 (TUSC5), mRNA [NM_172367]
509	A_33_P3291732	2,922	up	FAM125A	family with sequence similarity 125, member A [Source:HGNC Symbol;Acc:25153] [ENST00000529490]
510	A_23_P332713	2,922	up	ZFR2	Homo sapiens zinc finger RNA binding protein 2 (ZFR2), transcript variant 1, mRNA [NM_015174]
511	A_33_P3383381	2,921	up	SPHKAP	Homo sapiens SPHK1 interactor, AKAP domain containing (SPHKAP), transcript variant 1, mRNA [NM_001142644]
512	A_24_P212860	2,915	up	C9orf156	Homo sapiens chromosome 9 open reading frame 156 (C9orf156), mRNA [NM_016481]
513	A_33_P3405509	2,911	up	MAGEB5	melanoma antigen family B, 5 [Source:HGNC Symbol;Acc:23795] [ENST00000379029]
514	A_33_P3348086	2,911	up		ENK5_HUMAN (Q902F9) HERV-K_19p13,11 provirus ancestral Env polyprotein precursor (Envelope polyprotein) (HERV-K113 envelope protein) (EnvK5 protein) [Contains: Surface protein (SU); Transmembrane protein (TM)], partial (16%) [THC2503284]
515	A_33_P3358885	2,911	up	LOC100130913	Homo sapiens cDNA FLJ46498 fis, clone THYMU3029318, [AK128355]
516	A_33_P3285371	2,910	up		
517	A_32_P205053	2,910	up	UBXN10	UBX domain protein 10 [Source:HGNC Symbol;Acc:26354] [ENST00000375099]
518	A_33_P3220545	2,909	up	SLC6A19	Homo sapiens solute carrier family 6 (neutral amino acid transporter), member 19 (SLC6A19), mRNA [NM_001003841]
519	A_33_P3312030	2,906	up		
520	A_33_P3368203	2,906	up		Q5Z4F3_ORYSA (Q5Z4F3) Blue copper binding protein-like, partial (16%) [THC2673965]
521	A_24_P68068	2,904	up		Nanog homeobox pseudogene 1 [Source:HGNC Symbol;Acc:23099] [ENST00000530989]
522	A_23_P153662	2,904	up	LGALS14	Homo sapiens lectin, galactoside-binding, soluble, 14 (LGALS14), transcript variant 2, mRNA [NM_203471]
523	A_23_P128362	2,902	up	MYBPC1	Homo sapiens myosin binding protein C, slow type (MYBPC1), transcript variant 2, mRNA [NM_206819]
524	A_33_P3411980	2,900	up	ABI3BP	Homo sapiens mRNA; cDNA DKFZp667H216 (from clone DKFZp667H216), [AL833204]
525	A_33_P3309414	2,900	up	LOC643770	Homo sapiens hypothetical LOC643770 (LOC643770), non-coding RNA [NR_038383]
526	A_33_P3409655	2,899	up		
527	A_33_P3222380	2,899	up	AHNAK2	Homo sapiens AHNAK nucleoprotein 2 (AHNAK2), mRNA [NM_138420]
528	A_23_P90944	2,899	up	SCN7A	Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), mRNA [NM_002976]
529	A_24_P255845	2,898	up		
530	A_33_P3300217	2,892	up	MYLK3	Homo sapiens myosin light chain kinase 3 (MYLK3), mRNA [NM_182493]
531	A_23_P111978	2,892	up	KCNK9	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA [NM_016601]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
532	A_24_P175427	2,891	up	MRRF	Homo sapiens mitochondrial ribosome recycling factor (MRRF), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_199177]
533	A_33_P3261308	2,890	up		
534	A_23_P96165	2,890	up	C11orf80	Homo sapiens chromosome 11 open reading frame 80 (C11orf80), mRNA [NM_024650]
535	A_33_P3408752	2,886	up		forkhead box O6 [Source:HGNC Symbol;Acc:24814] [ENST00000372591]
536	A_33_P3358789	2,885	up		ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (5%) [THC2558186]
537	A_33_P3370265	2,876	up	LOC100508645	PREDICTED: Homo sapiens hypothetical protein LOC100508645 (LOC100508645), partial mRNA [XM_003120021]
538	A_33_P3412418	2,875	up		Homo sapiens cDNA FLJ40480 fis, clone TESTI2043313, [AK097799]
539	A_33_P3314401	2,874	up	CLDN16	Homo sapiens claudin 16 (CLDN16), mRNA [NM_006580]
540	A_33_P3321034	2,873	up	PLXNA4	Homo sapiens plexin A4 (PLXNA4), transcript variant 1, mRNA [NM_020911]
541	A_23_P207582	2,872	up	CCL16	Homo sapiens chemokine (C-C motif) ligand 16 (CCL16), mRNA [NM_004590]
542	A_32_P108889	2,872	up	DCLK1	Homo sapiens doublecortin-like kinase 1 (DCLK1), transcript variant 1, mRNA [NM_004734]
543	A_24_P409519	2,871	up	PTPN5	Homo sapiens protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched) (PTPN5), transcript variant 1, mRNA [NM_006906]
544	A_24_P14932	2,868	up	WDR52	Homo sapiens WD repeat domain 52 (WDR52), transcript variant 2, mRNA [NM_018338]
545	A_24_P272254	2,867	up	SPACA5	Homo sapiens sperm acrosome associated 5 (SPACA5), mRNA [NM_205856]
546	A_33_P3328312	2,866	up	HNF1A	Homo sapiens HNF1 homeobox A (HNF1A), mRNA [NM_000545]
547	A_33_P3362981	2,865	up	KCTD5	Homo sapiens potassium channel tetramerisation domain containing 5 (KCTD5), mRNA [NM_018992]
548	A_24_P75127	2,865	up		hemicentin 2 [Source:HGNC Symbol;Acc:21293] [ENST00000487727]
549	A_33_P3391578	2,865	up	RPL23AP64	Homo sapiens ribosomal protein L23a pseudogene 64 (RPL23AP64), non-coding RNA [NR_003040]
550	A_24_P377124	2,864	up	THPO	Homo sapiens thrombopoietin (THPO), transcript variant 1, mRNA [NM_000460]
551	A_33_P3369446	2,863	up		Homo sapiens cDNA FLJ41306 fis, clone BRAMY2042549, [AK123300]
552	A_33_P3222056	2,863	up		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E9PQU3] [ENST00000533322]
553	A_33_P3263938	2,861	up	LCN15	Homo sapiens lipocalin 15 (LCN15), mRNA [NM_203347]
554	A_33_P3414477	2,861	up	LOC729739	PREDICTED: Homo sapiens hypothetical LOC729739 (LOC729739), miscRNA [XR_109164]
555	A_23_P89302	2,859	up	CACNG1	Homo sapiens calcium channel, voltage-dependent, gamma subunit 1 (CACNG1), mRNA [NM_000727]
556	A_33_P3381996	2,858	up		chromosome 8 open reading frame 49 [Source:HGNC Symbol;Acc:32200] [ENST00000525043]
557	A_23_P395632	2,856	up	R3HDML	Homo sapiens R3H domain containing-like (R3HDML), mRNA [NM_178491]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
558	A_33_P3304754	2,855	up	TPP2	tripeptidyl peptidase II [Source:HGNC Symbol;Acc:12016] [ENST00000490010]
559	A_33_P3390387	2,853	up		
560	A_33_P3417437	2,851	up	CD164L2	Homo sapiens CD164 sialomucin-like 2 (CD164L2), mRNA [NM_207397]
561	A_33_P3404779	2,850	up	TCTEX1D4	Homo sapiens Tctex1 domain containing 4 (TCTEX1D4), mRNA [NM_001013632]
562	A_33_P3415255	2,850	up	VN1R1	Homo sapiens vomeronasal 1 receptor 1 (VN1R1), mRNA [NM_020633]
563	A_23_P306223	2,849	up	ARX	Homo sapiens aristaless related homeobox (ARX), mRNA [NM_139058]
564	A_24_P32139	2,847	up	HTR3E	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3, family member E (HTR3E), mRNA [NM_182589]
565	A_33_P3213726	2,847	up	ZNF585B	Homo sapiens zinc finger protein 585B (ZNF585B), mRNA [NM_152279]
566	A_33_P3263379	2,846	up	SNORD17	Homo sapiens small nucleolar RNA, C/D box 17 (SNORD17), small nucleolar RNA [NR_003045]
567	A_33_P3333787	2,846	up		
568	A_33_P3212102	2,845	up	SLC10A6	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 6 (SLC10A6), mRNA [NM_197965]
569	A_33_P3356182	2,845	up		
570	A_32_P217543	2,845	up		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:C9JG08] [ENST00000447166]
571	A_23_P73097	2,842	up	RGS20	Homo sapiens regulator of G-protein signaling 20 (RGS20), transcript variant 1, mRNA [NM_170587]
572	A_23_P131801	2,840	up	SGK2	Homo sapiens serum/glucocorticoid regulated kinase 2 (SGK2), transcript variant 1, mRNA [NM_170693]
573	A_33_P3320533	2,835	up	POLR1A	polymerase (RNA) I polypeptide A, 194kDa [Source:HGNC Symbol;Acc:17264] [ENST00000486964]
574	A_33_P3230161	2,835	up	GRIA2	Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), transcript variant 1, mRNA [NM_000826]
575	A_33_P3382758	2,834	up		BX404796 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CS0DM011YO11 5-PRIME, mRNA sequence [BX404796]
576	A_33_P3381621	2,834	up	PLB1	phospholipase B1 [Source:HGNC Symbol;Acc:30041] [ENST00000329020]
577	A_33_P3252316	2,833	up		
578	A_33_P3392460	2,832	up	LOC100128077	PREDICTED: Homo sapiens hypothetical LOC100128077 (LOC100128077), miscRNA [XR_108956]
579	A_33_P3311730	2,832	up		
580	A_23_P126528	2,832	up	KCNA10	Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 10 (KCNA10), mRNA [NM_005549]
581	A_24_P504621	2,832	up		
582	A_23_P106080	2,831	up	RNASE7	Homo sapiens ribonuclease, RNase A family, 7 (RNASE7), mRNA [NM_032572]
583	A_33_P3286121	2,829	up	LOC730159	Homo sapiens hypothetical protein LOC730159 (LOC730159), mRNA [NM_001195190]
584	A_33_P3390924	2,827	up		PREDICTED: Homo sapiens hypothetical LOC100127950 (LOC100127950), miscRNA [XR_110674]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
585	A_33_P3377719	2,823	up	LOC100129112	Homo sapiens cDNA FLJ41845 fis, clone NT2RI3003095, [AK123839]
586	A_23_P329962	2,823	up	SUN3	Homo sapiens Sad1 and UNC84 domain containing 3 (SUN3), transcript variant 1, mRNA [NM_001030019]
587	A_33_P3316329	2,823	up		
588	A_33_P3300800	2,822	up	GUCY2E	Homo sapiens guanylate cyclase 2E (GUCY2E), non-coding RNA [NR_024042]
589	A_24_P186608	2,821	up	DPY19L2P2	Homo sapiens dpy-19-like 2 pseudogene 2 (C, elegans) (DPY19L2P2), transcript variant 2, non-coding RNA [NR_003561]
590	A_33_P3262253	2,821	up		suppressor of variegation 4-20 homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:28405] [ENST00000539076]
591	A_33_P3531791	2,821	up	LOC728099	Homo sapiens cDNA clone IMAGE:4824569, [BC036362]
592	A_33_P3407618	2,819	up	AGSK1	Homo sapiens golgin subfamily A member 2-like (AGSK1), non-coding RNA [NR_026811]
593	A_32_P33114	2,817	up	KLB	Homo sapiens klotho beta (KLB), mRNA [NM_175737]
594	A_33_P3390107	2,816	up	RN18S1	Homo sapiens RNA, 18S ribosomal 1 (RN18S1), ribosomal RNA [NR_003286]
595	A_24_P110365	2,814	up		HCG1980662 [Source:UniProtKB/TrEMBL;Acc:Q86VH3] [ENST00000446344]
596	A_23_P163711	2,814	up	FAM57B	Homo sapiens family with sequence similarity 57, member B (FAM57B), mRNA [NM_031478]
597	A_23_P414958	2,810	up	PLXNC1	Homo sapiens plexin C1 (PLXNC1), transcript variant 1, mRNA [NM_005761]
598	A_32_P67526	2,810	up	PCDP1	Homo sapiens primary ciliary dyskinesia protein 1 (PCDP1), mRNA [NM_001029996]
599	A_33_P3230011	2,805	up	STOX1	Homo sapiens storkhead box 1 (STOX1), transcript variant 3, mRNA [NM_001130159]
600	A_33_P3248787	2,805	up		DB221055 TRACH3 Homo sapiens cDNA clone TRACH3011617 5', mRNA sequence [DB221055]
601	A_33_P3322348	2,803	up		cDNA FLJ46600 fis, clone THYMU3047144 [Source:UniProtKB/TrEMBL;Acc:Q6ZR66] [ENST00000374945]
602	A_33_P3298349	2,803	up	ART5	Homo sapiens ADP-ribosyltransferase 5 (ART5), transcript variant 1, mRNA [NM_053017]
603	A_23_P11005	2,803	up	ADAMTS7	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 7 (ADAMTS7), mRNA [NM_014272]
604	A_23_P34946	2,800	up	DIEXF	Homo sapiens digestive organ expansion factor homolog (zebrafish) (DIEXF), mRNA [NM_014388]
605	A_33_P3298455	2,799	up		CDNA FLJ20464 fis, clone KAT06158HCG1777549 [Source:UniProtKB/TrEMBL;Acc:Q9NX35] [ENST00000504184]
606	A_33_P3398111	2,799	up		chromosome 16 open reading frame 85 [Source:HGNC Symbol;Acc:33799] [ENST00000378416]
607	A_24_P275585	2,796	up	IQCH	Homo sapiens IQ motif containing H (IQCH), transcript variant 1, mRNA [NM_001031715]
608	A_33_P3369016	2,796	up		
609	A_23_P78795	2,795	up	MEIS3	Homo sapiens Meis homeobox 3 (MEIS3), transcript variant 2, mRNA [NM_001009813]
610	A_23_P77756	2,793	up	GALR2	Homo sapiens galanin receptor 2 (GALR2), mRNA [NM_003857]
611	A_24_P684183	2,792	up	SLC44A4	Homo sapiens solute carrier family 44, member 4 (SLC44A4), transcript variant 1, mRNA [NM_025257]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
612	A_33_P3238295	2,792	up	FAM66C	Homo sapiens family with sequence similarity 66, member C (FAM66C), non-coding RNA [NR_026788]
613	A_24_P109633	2,789	up	ITPK1	Homo sapiens inositol-tetrakisphosphate 1-kinase (ITPK1), transcript variant 3, mRNA [NM_001142594]
614	A_33_P3396578	2,789	up	GRK5	G protein-coupled receptor kinase 5 [Source:HGNC Symbol;Acc:4544] [ENST00000369106]
615	A_33_P3379811	2,789	up	C12orf77	Homo sapiens chromosome 12 open reading frame 77 (C12orf77), mRNA [NM_001101339]
616	A_24_P215240	2,788	up	ENKUR	Homo sapiens enkurin, TRPC channel interacting protein (ENKUR), mRNA [NM_145010]
617	A_33_P3298251	2,787	up		
618	A_32_P150645	2,785	up		EST00381 Fetal Brain, Bento Soares Homo sapiens cDNA clone HEFBA04, mRNA sequence [M78233]
619	A_33_P3320678	2,785	up	CLEC18C	Homo sapiens C-type lectin domain family 18, member C (CLEC18C), mRNA [NM_173619]
620	A_24_P15640	2,785	up		Homo sapiens chromosome 19 open reading frame 31, mRNA (cDNA clone MGC:168625 IMAGE:9021002), complete cds, [BC137009]
621	A_24_P169896	2,783	up		cDNA FLJ32655 fis, clone TESTI1000025, weakly similar to M,musculus testis-specific protein, DDC8 [Source:UniProtKB/TrEMBL;Acc:Q96MC4] [ENST00000475198]
622	A_32_P37495	2,783	up	LOC100506700	PREDICTED: Homo sapiens hypothetical LOC100506700 (LOC100506700), partial miscRNA [XR_110229]
623	A_33_P3221203	2,782	up	MMP13	Homo sapiens matrix metallopeptidase 13 (collagenase 3) (MMP13), mRNA [NM_002427]
624	A_24_P247026	2,782	up	FAM154B	Homo sapiens family with sequence similarity 154, member B (FAM154B), mRNA [NM_001008226]
625	A_33_P3325643	2,781	up	FLJ42418	Homo sapiens hypothetical LOC400941 (FLJ42418), non-coding RNA [NR_038369]
626	A_24_P121406	2,781	up	ZC3H13	Homo sapiens zinc finger CCCH-type containing 13 (ZC3H13), mRNA [NM_015070]
627	A_24_P282547	2,779	up	CFHR4	Homo sapiens complement factor H-related 4 (CFHR4), transcript variant 3, mRNA [NM_006684]
628	A_32_P118568	2,779	up	RFPL1-AS1	Homo sapiens RFPL1 antisense RNA 1 (non-protein coding) (RFPL1-AS1), antisense RNA [NR_002727]
629	A_23_P1904	2,778	up	MS4A2	Homo sapiens membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) (MS4A2), mRNA [NM_000139]
630	A_32_P11096	2,778	up	ZCCHC13	Homo sapiens zinc finger, CCHC domain containing 13 (ZCCHC13), mRNA [NM_203303]
631	A_33_P3314091	2,778	up		
632	A_24_P109887	2,775	up		Homo sapiens hypothetical LOC554207, mRNA (cDNA clone MGC:21504 IMAGE:3882600), complete cds, [BC031469]
633	A_33_P3323486	2,774	up		Synthetic construct DNA, clone: pF1KE0827, Homo sapiens OR4A13P gene for Putative olfactory receptor, family 4, subfamily A, member 13, without stop codon, in Flexi system, [AB529256]
634	A_33_P3407643	2,772	up	C11orf34	Homo sapiens chromosome 11 open reading frame 34 (C11orf34), mRNA [NM_001145024]
635	A_33_P3380992	2,771	up	AKR1B15	Homo sapiens aldo-keto reductase family 1, member B15 (AKR1B15), mRNA [NM_001080538]
636	A_33_P3384628	2,769	up		
637	A_33_P3773195	2,767	up	LOC285762	Homo sapiens cDNA FLJ39782 fis, clone SPLEN2002175, [AK097101]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
638	A_33_P3241388	2,765	up	SLC4A5	Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant a, mRNA [NM_021196]
639	A_33_P3340828	2,765	up		PREDICTED: Homo sapiens similar to hCG2041342 (LOC100128935), mRNA [XM_001723580]
640	A_33_P3388391	2,762	up	GJB4	Homo sapiens gap junction protein, beta 4, 30,3kDa (GJB4), mRNA [NM_153212]
641	A_24_P936010	2,762	up		Homo sapiens clone DNA172120 micronovel (UNQ9353) mRNA, complete cds, [AY358253]
642	A_24_P281908	2,762	up	CUX2	Homo sapiens cut-like homeobox 2 (CUX2), mRNA [NM_015267]
643	A_33_P3243307	2,761	up	LOC100128281	Homo sapiens cDNA FLJ46495 fis, clone THYMU3028461, [AK128353]
644	A_33_P3764663	2,761	up	MKRN9P	Homo sapiens makorin ring finger protein pseudogene 6, mRNA (cDNA clone IMAGE:5278542), [BC067894]
645	A_33_P3277532	2,759	up	LAMC3	Homo sapiens laminin, gamma 3 (LAMC3), mRNA [NM_006059]
646	A_33_P3423171	2,757	up	WDR6	Homo sapiens WD repeat domain 6 (WDR6), mRNA [NM_018031]
647	A_33_P3282018	2,755	up	MCF2L	Homo sapiens MCF,2 cell line derived transforming sequence-like (MCF2L), transcript variant 2, mRNA [NM_024979]
648	A_33_P3309110	2,754	up	LOC100506713	Homo sapiens hypothetical LOC100506713 (LOC100506713), non-coding RNA [NR_040089]
649	A_33_P3214825	2,753	up		Homo sapiens clone DNA119530 VLCS3029 (UNQ3029) mRNA, complete cds, [AY358806]
650	A_23_P47665	2,752	up	HBE1	Homo sapiens hemoglobin, epsilon 1 (HBE1), mRNA [NM_005330]
651	A_33_P3292130	2,752	up		Q2JG47_FRASC (Q2JG47) Methyltransferase type 11, partial (6%) [THC2566648]
652	A_33_P3265024	2,752	up	ST5	Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 1, mRNA [NM_005418]
653	A_24_P211558	2,747	up	PATZ1	Homo sapiens POZ (BTB) and AT hook containing zinc finger 1 (PATZ1), transcript variant 4, mRNA [NM_032051]
654	A_33_P3356092	2,746	up	BTBD9	Homo sapiens BTB (POZ) domain containing 9 (BTBD9), transcript variant 1, mRNA [NM_052893]
655	A_33_P3361388	2,746	up	MYCBPAP	Homo sapiens MYCBP associated protein (MYCBPAP), mRNA [NM_032133]
656	A_33_P3389332	2,746	up	LOC100128531	Homo sapiens hypothetical LOC100128531 (LOC100128531), non-coding RNA [NR_038941]
657	A_33_P3350202	2,744	up	MOCS3	Homo sapiens molybdenum cofactor synthesis 3 (MOCS3), mRNA [NM_014484]
658	A_33_P3281765	2,741	up		
659	A_23_P144337	2,741	up	CCRN4L	Homo sapiens CCR4 carbon catabolite repression 4-like (S, cerevisiae) (CCRN4L), mRNA [NM_012118]
660	A_33_P3323463	2,738	up	HSPA8	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:5241] [ENST00000532091]
661	A_23_P128351	2,738	up	EFCAB4B	Homo sapiens EF-hand calcium binding domain 4B (EFCAB4B), transcript variant 3, mRNA [NM_032680]
662	A_24_P331779	2,738	up	RSPH4A	Homo sapiens radial spoke head 4 homolog A (Chlamydomonas) (RSPH4A), transcript variant 1, mRNA [NM_001010892]
663	A_33_P3389842	2,737	up	PROM1	Homo sapiens prominin 1 (PROM1), transcript variant 6, mRNA [NM_001145850]
664	A_33_P3489228	2,736	up	PTPN20A	Homo sapiens protein tyrosine phosphatase, non-receptor type 20A (PTPN20A), transcript variant 2, mRNA [NM_001042387]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
665	A_33_P3401284	2,736	up	RMRP	Homo sapiens RNA component of mitochondrial RNA processing endoribonuclease (RMRP), RNase MRP RNA [NR_003051]
666	A_33_P3743432	2,736	up	DEFA8P	Homo sapiens defensin alpha 8 (DEFA8P) pseudogene mRNA, complete sequence, [AY746433]
667	A_33_P3295148	2,735	up		Homo sapiens cDNA FLJ46292 fis, clone TESTI4033177, highly similar to Dual specificity protein phosphatase 8 (EC 3,1,3,48), [AK128169]
668	A_33_P3289845	2,733	up	IGFL1	Homo sapiens IGF-like family member 1 (IGFL1), mRNA [NM_198541]
669	A_23_P252817	2,733	up	SST	Homo sapiens somatostatin (SST), mRNA [NM_001048]
670	A_33_P3378935	2,730	up	RBM14	Homo sapiens mRNA for RNA binding motif protein 14 variant protein, [AB209007]
671	A_23_P138089	2,729	up	MPZ	Homo sapiens myelin protein zero (MPZ), mRNA [NM_000530]
672	A_33_P3274754	2,729	up	LOC100131434	Homo sapiens hypothetical LOC100131434 (LOC100131434), non-coding RNA [NR_027455]
673	A_32_P48244	2,728	up	ZNF100	zinc finger protein 100 [Source:HGNC Symbol;Acc:12880] [ENST00000358296]
674	A_23_P92517	2,727	up	TTC29	Homo sapiens tetratricopeptide repeat domain 29 (TTC29), mRNA [NM_031956]
675	A_24_P6674	2,725	up	WDR31	Homo sapiens WD repeat domain 31 (WDR31), transcript variant 1, mRNA [NM_001012361]
676	A_24_P723735	2,725	up		
677	A_33_P3233040	2,723	up	SERPINB11	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 11 (gene/pseudogene) (SERPINB11), mRNA [NM_080475]
678	A_33_P3315325	2,723	up	ANKRD46	ankyrin repeat domain 46 [Source:HGNC Symbol;Acc:27229] [ENST00000520552]
679	A_23_P333029	2,722	up	C8orf47	Homo sapiens chromosome 8 open reading frame 47 (C8orf47), transcript variant 1, mRNA [NM_173549]
680	A_33_P3289576	2,721	up	EFHC2	Homo sapiens EF-hand domain (C-terminal) containing 2 (EFHC2), mRNA [NM_025184]
681	A_33_P3297244	2,720	up	GAS2L2	Homo sapiens growth arrest-specific 2 like 2 (GAS2L2), mRNA [NM_139285]
682	A_33_P3262108	2,719	up		
683	A_33_P3389779	2,719	up	WDR33	WD repeat domain 33 [Source:HGNC Symbol;Acc:25651] [ENST00000408998]
684	A_33_P3273125	2,718	up	FAM106CP	Homo sapiens family with sequence similarity 106, member C, pseudogene (FAM106CP), non-coding RNA [NR_026810]
685	A_33_P3287636	2,715	up		Human mRNA for T cell receptor V alpha gene segment V-alpha-w23, clone IGRa01, [X58736]
686	A_33_P3366431	2,713	up	LCN1	Homo sapiens lipocalin 1 (tear prealbumin) (LCN1), mRNA [NM_002297]
687	A_33_P3338788	2,713	up		
688	A_23_P130961	2,712	up	ELANE	Homo sapiens elastase, neutrophil expressed (ELANE), mRNA [NM_001972]
689	A_23_P23829	2,712	up	CD34	Homo sapiens CD34 molecule (CD34), transcript variant 2, mRNA [NM_001773]
690	A_33_P3270519	2,712	up	FAM40A	Homo sapiens family with sequence similarity 40, member A (FAM40A), mRNA [NM_033088]
691	A_23_P412427	2,710	up	NS3BP	PREDICTED: Homo sapiens NS3BP (NS3BP), miscRNA [XR_109071]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
692	A_23_P349025	2,709	up	SAMD15	Homo sapiens sterile alpha motif domain containing 15 (SAMD15), mRNA [NM_001010860]
693	A_33_P3401003	2,707	up	C7orf71	Homo sapiens chromosome 7 open reading frame 71 (C7orf71), mRNA [NM_001145531]
694	A_33_P3345350	2,706	up	DRGX	Homo sapiens dorsal root ganglia homeobox (DRGX), mRNA [NM_001080520]
695	A_23_P308136	2,706	up	TRIM50	Homo sapiens tripartite motif containing 50 (TRIM50), mRNA [NM_178125]
696	A_33_P3208995	2,704	up		Homo sapiens cDNA clone IMAGE:40000318, [BC100776]
697	A_33_P3407990	2,703	up	LOC100130193	Homo sapiens cDNA FLJ38783 fis, clone LIVER2001191, [AK096102]
698	A_32_P46603	2,703	up	VWA3B	Homo sapiens von Willebrand factor A domain containing 3B (VWA3B), mRNA [NM_144992]
699	A_23_P5018	2,702	up	LOC80054	Homo sapiens hypothetical LOC80054 (LOC80054), non-coding RNA [NR_026887]
700	A_33_P3272281	2,702	up		Homo sapiens cDNA FLJ44874 fis, clone BRAMY2025495, [AK126822]
701	A_33_P3209254	2,701	up	RPS16P5	Homo sapiens cDNA FLJ40618 fis, clone THYMU2013089, [AK097937]
702	A_33_P3283734	2,698	up		
703	A_23_P57492	2,698	up	SLC5A4	Homo sapiens solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4), mRNA [NM_014227]
704	A_33_P3383236	2,695	up	C2orf62	Homo sapiens chromosome 2 open reading frame 62 (C2orf62), mRNA [NM_198559]
705	A_33_P3346766	2,694	up	UGT2A2	Homo sapiens UDP glucuronosyltransferase 2 family, polypeptide A2 (UGT2A2), mRNA [NM_001105677]
706	A_24_P127691	2,694	up	DNAH14	dynein, axonemal, heavy chain 14 [Source:HGNC Symbol;Acc:2945] [ENST00000495456]
707	A_23_P349398	2,694	up	ZAR1	Homo sapiens zygote arrest 1 (ZAR1), mRNA [NM_175619]
708	A_33_P3209283	2,693	up	SASH1	SAM and SH3 domain containing 1 [Source:HGNC Symbol;Acc:19182] [ENST00000367469]
709	A_33_P3230541	2,693	up	MPRIP	myosin phosphatase Rho interacting protein [Source:HGNC Symbol;Acc:30321] [ENST00000395806]
710	A_33_P3800496	2,692	up	SNORA46	DKFZp686L14114_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686L14114 5', mRNA sequence [BX470739]
711	A_33_P3341686	2,691	up	XIST	Homo sapiens X (inactive)-specific transcript (non-protein coding) (XIST), non-coding RNA [NR_001564]
712	A_23_P66432	2,691	up	TTYH2	Homo sapiens tweety homolog 2 (Drosophila) (TTYH2), transcript variant 1, mRNA [NM_032646]
713	A_24_P320163	2,691	up	PPBPL2	Homo sapiens pro-platelet basic protein-like 2 (PPBPL2), non-coding RNA [NR_026769]
714	A_32_P332551	2,690	up	C13orf30	Homo sapiens chromosome 13 open reading frame 30 (C13orf30), mRNA [NM_182508]
715	A_33_P3390264	2,690	up	OR10W1	Homo sapiens olfactory receptor, family 10, subfamily W, member 1 (OR10W1), mRNA [NM_207374]
716	A_23_P211973	2,687	up	NEK11	Homo sapiens NIMA (never in mitosis gene a)- related kinase 11 (NEK11), transcript variant 1, mRNA [NM_024800]
717	A_24_P359322	2,686	up	C21orf49	Homo sapiens chromosome 21 open reading frame 49 (C21orf49), transcript variant 1, non-coding RNA [NR_024622]
718	A_33_P3266783	2,685	up		Q66I89_BRARE (Q66I89) PQ loop repeat containing 3, partial (6%) [THC2736258]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
719	A_24_P301547	2,683	up	C17orf80	Homo sapiens chromosome 17 open reading frame 80 (C17orf80), transcript variant 1, mRNA [NM_017941]
720	A_23_P27709	2,683	up	CGB2	Homo sapiens chorionic gonadotropin, beta polypeptide 2 (CGB2), mRNA [NM_033378]
721	A_33_P3376131	2,683	up	NT5DC4	Homo sapiens 5'-nucleotidase domain containing 4, mRNA (cDNA clone IMAGE:5163442), partial cds, [BC041437]
722	A_33_P3371553	2,682	up	FLJ32756	Homo sapiens cDNA FLJ32756 fis, clone TESTI2001758, [AK057318]
723	A_33_P3364721	2,681	up		
724	A_33_P3304794	2,681	up		Homo sapiens cDNA FLJ39005 fis, clone NT2RI2024496, [AK096324]
725	A_33_P3356413	2,677	up		MMFIBRLNA fibrillarin {Mus musculus} (exp=-1; wgp=0; cg=0), partial (8%) [THC2638856]
726	A_32_P199884	2,677	up	HORMAD1	Homo sapiens HORMA domain containing 1 (HORMAD1), transcript variant 1, mRNA [NM_032132]
727	A_33_P3382236	2,677	up	KIAA1598	Homo sapiens KIAA1598 (KIAA1598), transcript variant 2, mRNA [NM_018330]
728	A_33_P3294103	2,676	up		
729	A_23_P96633	2,675	up	CXorf48	Homo sapiens chromosome X open reading frame 48 (CXorf48), transcript variant 1, mRNA [NM_001031705]
730	A_33_P3402211	2,670	up	LOC100506220	PREDICTED: Homo sapiens hypothetical LOC100506220 (LOC100506220), partial miscRNA [XR_110895]
731	A_33_P3331731	2,669	up		
732	A_32_P182394	2,668	up	ZNF77	Homo sapiens zinc finger protein 77 (ZNF77), mRNA [NM_021217]
733	A_23_P202034	2,668	up	GUCY2GP	Homo sapiens guanylate cyclase 2G homolog (mouse), pseudogene (GUCY2GP), non-coding RNA [NR_028134]
734	A_33_P3423185	2,667	up	DPF3	Homo sapiens cDNA FLJ14079 fis, clone HEMBB1002134, weakly similar to ZINC-FINGER PROTEIN NEURO-D4, [AK024141]
735	A_24_P16856	2,667	up	AKAP17A	A kinase (PRKA) anchor protein 17A [Source:HGNC Symbol;Acc:18783] [ENST00000381261]
736	A_24_P271323	2,667	up	SLC2A10	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), mRNA [NM_030777]
737	A_23_P377750	2,667	up	FGF10	Homo sapiens fibroblast growth factor 10 (FGF10), mRNA [NM_004465]
738	A_33_P3289123	2,666	up	DCLK3	Homo sapiens doublecortin-like kinase 3 (DCLK3), mRNA [NM_033403]
739	A_23_P4387	2,665	up	KRT24	Homo sapiens keratin 24 (KRT24), mRNA [NM_019016]
740	A_33_P3314952	2,665	up	TRPV1	Homo sapiens transient receptor potential cation channel, subfamily V, member 1 (TRPV1), transcript variant 3, mRNA [NM_080706]
741	A_23_P133842	2,664	up	HIST1H1T	Homo sapiens histone cluster 1, H1t (HIST1H1T), mRNA [NM_005323]
742	A_23_P311632	2,664	up	NLRP6	Homo sapiens NLR family, pyrin domain containing 6 (NLRP6), mRNA [NM_138329]
743	A_33_P3268035	2,661	up	LYZL1	Homo sapiens lysozyme-like 1 (LYZL1), mRNA [NM_032517]
744	A_33_P3369799	2,661	up	SLC35D3	Homo sapiens solute carrier family 35, member D3 (SLC35D3), mRNA [NM_001008783]
745	A_33_P3393667	2,658	up		T cell receptor alpha variable 1-1 [Source:HGNC Symbol;Acc:12101] [ENST00000542354]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
746	A_23_P137504	2,656	up	ZBTB37	Homo sapiens zinc finger and BTB domain containing 37 (ZBTB37), transcript variant 2, mRNA [NM_032522]
747	A_33_P3421530	2,656	up	HMCN2	PREDICTED: Homo sapiens hemicentin-2-like (LOC100292387), mRNA [XM_002346203]
748	A_23_P307860	2,655	up	SVOPL	Homo sapiens SVOP-like (SVOPL), transcript variant 2, mRNA [NM_174959]
749	A_33_P3366179	2,655	up		
750	A_24_P364057	2,654	up	C11orf70	Homo sapiens chromosome 11 open reading frame 70 (C11orf70), transcript variant 1, mRNA [NM_032930]
751	A_33_P3415310	2,654	up		
752	A_24_P564030	2,654	up	BTBD8	Homo sapiens BTB (POZ) domain containing 8 (BTBD8), mRNA [NM_183242]
753	A_23_P413760	2,653	up	P2RX5	Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 5 (P2RX5), transcript variant 2, mRNA [NM_175080]
754	A_23_P74870	2,652	up	C1orf129	Homo sapiens chromosome 1 open reading frame 129 (C1orf129), transcript variant 2, mRNA [NM_025063]
755	A_32_P101779	2,651	up	SEC14L3	Homo sapiens SEC14-like 3 (S, cerevisiae) (SEC14L3), mRNA [NM_174975]
756	A_33_P3215834	2,651	up	SORCS2	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA [NM_020777]
757	A_33_P3384695	2,650	up	NCALD	Homo sapiens mRNA for Neurocalcin delta variant protein, [AB209015]
758	A_23_P167882	2,650	up	IL17F	Homo sapiens interleukin 17F (IL17F), mRNA [NM_052872]
759	A_32_P140489	2,649	up	GDF6	Homo sapiens growth differentiation factor 6 (GDF6), mRNA [NM_001001557]
760	A_33_P3386746	2,649	up	C10orf112	chromosome 10 open reading frame 112 [Source:HGNC Symbol;Acc:24331] [ENST00000454679]
761	A_33_P3228739	2,646	up	LRRC3C	Homo sapiens leucine rich repeat containing 3C (LRRC3C), mRNA [NM_001195545]
762	A_33_P3329149	2,646	up	CDK13	Homo sapiens cyclin-dependent kinase 13 (CDK13), transcript variant 2, mRNA [NM_031267]
763	A_24_P336137	2,644	up	C22orf23	Homo sapiens chromosome 22 open reading frame 23 (C22orf23), transcript variant 1, mRNA [NM_032561]
764	A_33_P3232742	2,644	up		
765	A_33_P3339624	2,644	up	C6orf127	Homo sapiens chromosome 6 open reading frame 127 (C6orf127), mRNA [NM_001010886]
766	A_33_P3282205	2,643	up		Homo sapiens cDNA: FLJ22766 fis, clone KAIA1188, [AK026419]
767	A_33_P3238402	2,641	up		
768	A_33_P3237899	2,640	up	CHN2	Homo sapiens chimerin (chimaerin) 2 (CHN2), transcript variant 2, mRNA [NM_004067]
769	A_33_P3463924	2,640	up	LOC57399	Homo sapiens uncharacterized gastric protein ZA52P mRNA, complete cds, [AF264626]
770	A_33_P3287113	2,640	up	KIAA1530	KIAA1530 [Source:HGNC Symbol;Acc:29304] [ENST00000296312]
771	A_33_P3232478	2,639	up	CACNA2D1	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA [NM_000722]
772	A_33_P3413667	2,638	up	ABL2	Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 2 (ABL2), transcript variant e, mRNA [NM_001136001]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
773	A_23_P129425	2,637	up	TSNAXIP1	Homo sapiens translin-associated factor X interacting protein 1 (TSNAXIP1), mRNA [NM_018430]
774	A_32_P204980	2,636	up	FBXO39	Homo sapiens F-box protein 39 (FBXO39), mRNA [NM_153230]
775	A_33_P3415395	2,636	up	SPTLC3	Homo sapiens serine palmitoyltransferase, long chain base subunit 3 (SPTLC3), mRNA [NM_018327]
776	A_33_P3346327	2,635	up	KGFLP1	Homo sapiens keratinocyte growth factor-like protein 1 (KGFLP1), non-coding RNA [NR_003674]
777	A_33_P3401179	2,635	up		
778	A_23_P142187	2,634	up	HIF3A	Homo sapiens hypoxia inducible factor 3, alpha subunit (HIF3A), transcript variant 2, mRNA [NM_022462]
779	A_33_P3336462	2,634	up		Homo sapiens cDNA FLJ41306 fis, clone BRAMY2042549, [AK123300]
780	A_33_P3422968	2,632	up	DNAH6	Homo sapiens dynein, axonemal, heavy chain 6 (DNAH6), mRNA [NM_001370]
781	A_33_P3332521	2,631	up	PCDHA3	Homo sapiens protocadherin alpha 3 (PCDHA3), transcript variant 2, mRNA [NM_031497]
782	A_23_P121885	2,628	up	ROPN1L	Homo sapiens rhophilin associated tail protein 1-like (ROPN1L), transcript variant 1, mRNA [NM_031916]
783	A_33_P3247559	2,628	up	FNDC7	Homo sapiens fibronectin type III domain containing 7 (FNDC7), mRNA [NM_001144937]
784	A_33_P3280003	2,628	up	HERC2	Homo sapiens hect domain and RLD 2 (HERC2), mRNA [NM_004667]
785	A_24_P340800	2,627	up	ZNF621	Homo sapiens zinc finger protein 621 (ZNF621), transcript variant 1, mRNA [NM_198484]
786	A_24_P63078	2,625	up	YSK4	Homo sapiens YSK4 Sps1/Ste20-related kinase homolog (S, cerevisiae) (YSK4), transcript variant 1, mRNA [NM_025052]
787	A_33_P3481113	2,623	up	CECR3	Homo sapiens cat eye syndrome chromosome region, candidate 3 (non-protein coding) (CECR3), non-coding RNA [NR_038398]
788	A_33_P3212769	2,623	up	LOC100132686	Homo sapiens hypothetical LOC100132686, mRNA (cDNA clone MGC:24147 IMAGE:4702473), complete cds, [BC020894]
789	A_33_P3242688	2,623	up		
790	A_33_P3397127	2,623	up		Homo sapiens mRNA for T cell receptor beta variable 6, partial cds, clone: un 226, [AB306238]
791	A_23_P342709	2,622	up	FBXO15	Homo sapiens F-box protein 15 (FBXO15), transcript variant 1, mRNA [NM_152676]
792	A_32_P163458	2,622	up	SPDYE3	Homo sapiens speedy homolog E3 (Xenopus laevis) (SPDYE3), mRNA [NM_001004351]
793	A_32_P404549	2,620	up	CCDC39	Homo sapiens coiled-coil domain containing 39 (CCDC39), mRNA [NM_181426]
794	A_33_P3384052	2,620	up	RAX	Homo sapiens retina and anterior neural fold homeobox (RAX), mRNA [NM_013435]
795	A_33_P3651948	2,619	up	NEO1	Homo sapiens neogenin 1 (NEO1), transcript variant 1, mRNA [NM_002499]
796	A_33_P3321533	2,618	up		Q6DGZ4_BRARE (Q6DGZ4) Zgc:92710, partial (56%) [THC2671740]
797	A_33_P3264188	2,618	up	OR2D3	Homo sapiens olfactory receptor, family 2, subfamily D, member 3 (OR2D3), mRNA [NM_001004684]
798	A_33_P3221898	2,617	up	LOC339240	Homo sapiens keratin pseudogene (LOC339240), non-coding RNA [NR_001443]
799	A_33_P3230841	2,616	up	DUPD1	Homo sapiens dual specificity phosphatase and pro isomerase domain containing 1 (DUPD1), mRNA [NM_001003892]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
800	A_32_P423691	2,613	up	ADIG	Homo sapiens adipogenin (ADIG), mRNA [NM_001018082]
801	A_32_P203066	2,612	up	LOC100506955	PREDICTED: Homo sapiens hypothetical LOC100506955 (LOC100506955), partial miscRNA [XR_109782]
802	A_24_P400130	2,612	up	KRTAP7-1	Homo sapiens keratin associated protein 7-1 (gene/pseudogene) (KRTAP7-1), mRNA [NM_181606]
803	A_32_P319858	2,611	up	NKPD1	Homo sapiens NTPase, KAP family P-loop domain containing 1 (NKPD1), mRNA [NM_198478]
804	A_24_P254084	2,609	up	ZNF69	Homo sapiens zinc finger protein 69 (ZNF69), mRNA [NM_021915]
805	A_33_P3313810	2,607	up	CELA1	Homo sapiens chymotrypsin-like elastase family, member 1 (CELA1), mRNA [NM_001971]
806	A_23_P369343	2,606	up	KLK8	Homo sapiens kallikrein-related peptidase 8 (KLK8), transcript variant 2, mRNA [NM_144505]
807	A_33_P3244808	2,606	up	BEST4	Homo sapiens bestrophin 4 (BEST4), mRNA [NM_153274]
808	A_23_P377411	2,606	up	LOC100133130	Homo sapiens clone FLB4246 PRO1102 mRNA, complete cds, [AF130105]
809	A_33_P3324228	2,606	up		similar to hCG1645603 (LOC732275), non-coding RNA [Source:RefSeq DNA;Acc:NR_024406] [ENST00000304488]
810	A_33_P3260014	2,605	up	TPO	Homo sapiens thyroid peroxidase (TPO), transcript variant 4, mRNA [NM_175721]
811	A_23_P250228	2,603	up	HYAL4	Homo sapiens hyaluronoglucosaminidase 4 (HYAL4), mRNA [NM_012269]
812	A_33_P3386770	2,603	up		PREDICTED: Homo sapiens putative IQ motif and ankyrin repeat domain-containing protein LOC642574-like (LOC100508128), mRNA [XM_003120088]
813	A_33_P3228499	2,602	up		
814	A_24_P892494	2,601	up	LOC285548	Homo sapiens hypothetical LOC285548 (LOC285548), non-coding RNA [NR_015450]
815	A_33_P3309506	2,601	up	SEBOX	Homo sapiens SEBOX homeobox (SEBOX), mRNA [NM_001080837]
816	A_33_P3227217	2,601	up	SNORA81	Homo sapiens small nucleolar RNA, H/ACA box 81 (SNORA81), small nucleolar RNA [NR_002989]
817	A_23_P87279	2,600	up	TRPM5	Homo sapiens transient receptor potential cation channel, subfamily M, member 5 (TRPM5), mRNA [NM_014555]
818	A_23_P119634	2,599	up	UPK1A	Homo sapiens uroplakin 1A (UPK1A), mRNA [NM_007000]
819	A_32_P105825	2,599	up	MPPED2	Homo sapiens metallophosphoesterase domain containing 2 (MPPED2), transcript variant 1, mRNA [NM_001584]
820	A_23_P77908	2,599	up	SLC47A2	Homo sapiens solute carrier family 47, member 2 (SLC47A2), transcript variant 1, mRNA [NM_152908]
821	A_33_P3233764	2,597	up	LATS1	Homo sapiens LATS, large tumor suppressor, homolog 1 (Drosophila) (LATS1), mRNA [NM_004690]
822	A_33_P3394312	2,596	up	OR2A2	Homo sapiens olfactory receptor, family 2, subfamily A, member 2 (OR2A2), mRNA [NM_001005480]
823	A_33_P3325653	2,592	up		GB
824	A_33_P3215529	2,592	up	TJP2	Homo sapiens tight junction protein ZO-2 isoform C mRNA, partial cds, [AF083893]
825	A_32_P102519	2,591	up	LOC541473	Homo sapiens FK506 binding protein 6, 36kDa pseudogene (LOC541473), non-coding RNA [NR_003602]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
826	A_33_P3418952	2,591	up	ZDHHC15	Homo sapiens zinc finger, DHHC-type containing 15 (ZDHHC15), transcript variant 3, mRNA [NM_001146257]
827	A_33_P3306823	2,591	up	ZNF846	Homo sapiens zinc finger protein 846 (ZNF846), mRNA [NM_001077624]
828	A_23_P151895	2,587	up	CILP	Homo sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA [NM_003613]
829	A_33_P3234124	2,587	up	FAM132B	family with sequence similarity 132, member B [Source:HGNC Symbol;Acc:26727] [ENST00000481917]
830	A_23_P203665	2,584	up	ACER3	Homo sapiens alkaline ceramidase 3 (ACER3), mRNA [NM_018367]
831	A_33_P3323902	2,583	up	DEFB130	Homo sapiens defensin, beta 130 (DEFB130), mRNA [NM_001037804]
832	A_33_P3328621	2,583	up	LOC100132147	Homo sapiens cDNA clone IMAGE:4816083, partial cds, [BC036435]
833	A_24_P772488	2,583	up	PLXNA4	Homo sapiens plexin A4 (PLXNA4), transcript variant 1, mRNA [NM_020911]
834	A_33_P3303361	2,582	up	LOC402269	PREDICTED: Homo sapiens hypothetical protein LOC402269 (LOC402269), mRNA [XM_377941]
835	A_23_P375524	2,582	up	LCE1D	Homo sapiens late cornified envelope 1D (LCE1D), mRNA [NM_178352]
836	A_33_P3413325	2,581	up		Homo sapiens mRNA; cDNA DKFZp781N1049 (from clone DKFZp781N1049), [CR627384]
837	A_33_P3258279	2,578	up	NTM	Homo sapiens neurotrimin (NTM), transcript variant 4, mRNA [NM_001144059]
838	A_23_P30693	2,577	up	PLG	Homo sapiens plasminogen (PLG), transcript variant 1, mRNA [NM_000301]
839	A_33_P3265714	2,576	up	C2orf61	Homo sapiens chromosome 2 open reading frame 61 (C2orf61), transcript variant 2, mRNA [NM_173649]
840	A_33_P3235147	2,575	up	DLX5	Homo sapiens distal-less homeobox 5 (DLX5), mRNA [NM_005221]
841	A_32_P385667	2,575	up	MAGEB10	Homo sapiens melanoma antigen family B, 10 (MAGEB10), mRNA [NM_182506]
842	A_33_P3210303	2,575	up		Synthetic construct Homo sapiens gateway clone IMAGE:100021983 3' read WFS1 mRNA, [CU688821]
843	A_33_P3359713	2,575	up		ik35e10,y5 HR85 islet Homo sapiens cDNA clone IMAGE:5783130 5' similar to SW:TCPZ_HUMAN P40227 T-COMPLEX PROTEIN 1, ZETA SUBUNIT ;, mRNA sequence [CK825926]
844	A_23_P65302	2,574	up	SPACA7	Homo sapiens sperm acrosome associated 7 (SPACA7), mRNA [NM_145248]
845	A_33_P3251727	2,573	up	RYR2	Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA [NM_001035]
846	A_33_P3234949	2,572	up	GRID1	Homo sapiens glutamate receptor, ionotropic, delta 1 (GRID1), mRNA [NM_017551]
847	A_33_P3390246	2,572	up		Homo sapiens cDNA FLJ41707 fis, clone HLUNG2010464, [AK123701]
848	A_23_P152330	2,569	up	DOC2A	Homo sapiens double C2-like domains, alpha (DOC2A), mRNA [NM_003586]
849	A_23_P419503	2,567	up	LRRC4B	Homo sapiens leucine rich repeat containing 4B (LRRC4B), mRNA [NM_001080457]
850	A_33_P3412428	2,567	up	ADAM32	Homo sapiens ADAM metallopeptidase domain 32 (ADAM32), mRNA [NM_145004]
851	A_32_P530933	2,565	up	PYGO1	Homo sapiens pygopus homolog 1 (Drosophila) (PYGO1), mRNA [NM_015617]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
852	A_33_P3367541	2,565	up		ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (6%) [THC2681728]
853	A_24_P280497	2,564	up	FBRSL1	Homo sapiens fibrosin-like 1 (FBRSL1), mRNA [NM_001142641]
854	A_33_P3630780	2,564	up	LOC286058	Homo sapiens mRNA; cDNA DKFZp686J2011 (from clone DKFZp686J2011), [AL833160]
855	A_33_P3281041	2,563	up		NUD16_HUMAN (Q96DE0) Nucleoside diphosphate-linked moiety X motif 16 (Nudix motif 16) , partial (70%) [THC2710983]
856	A_23_P82975	2,560	up	VPS13B	Homo sapiens vacuolar protein sorting 13 homolog B (yeast) (VPS13B), transcript variant 4, mRNA [NM_181661]
857	A_33_P3303617	2,559	up		Homo sapiens clone HQ0255 PRO0255 mRNA, complete cds, [AF090909]
858	A_33_P3359513	2,558	up		Q6XBG3_MOUSE (Q6XBG3) ATP-binding cassette transporter sub-family A member 14, partial (7%) [THC2732607]
859	A_24_P106542	2,554	up	RSPO3	Homo sapiens R-spondin 3 (RSPO3), mRNA [NM_032784]
860	A_33_P3422265	2,554	up	LOC729305	PREDICTED: Homo sapiens hypothetical LOC729305 (LOC729305), partial miscRNA [XR_114546]
861	A_23_P359588	2,554	up	PCDHGB4	Homo sapiens protocadherin gamma subfamily B, 4 (PCDHGB4), transcript variant 2, mRNA [NM_032098]
862	A_33_P3321871	2,554	up	LOC339902	Homo sapiens hCG1813818 (LOC339902), non-coding RNA [NR_038862]
863	A_33_P3337921	2,554	up	LOC727944	PREDICTED: Homo sapiens hypothetical LOC727944, transcript variant 1 (LOC727944), partial miscRNA [XR_109991]
864	A_33_P3346966	2,552	up	SPAG16	Homo sapiens sperm associated antigen 16 (SPAG16), transcript variant 1, mRNA [NM_024532]
865	A_23_P390665	2,552	up	VWA3A	Homo sapiens von Willebrand factor A domain containing 3A (VWA3A), mRNA [NM_173615]
866	A_24_P66312	2,551	up	KRTAP12-1	Homo sapiens keratin associated protein 12-1 (KRTAP12-1), mRNA [NM_181686]
867	A_32_P14721	2,551	up	DNAH12	Homo sapiens dynein, axonemal, heavy chain 12 (DNAH12), transcript variant 1, mRNA [NM_178504]
868	A_33_P3420496	2,550	up	SNORA53	Homo sapiens small nucleolar RNA, H/ACA box 53 (SNORA53), small nucleolar RNA [NR_003015]
869	A_24_P93896	2,550	up	CNNM2	Homo sapiens cyclin M2 (CNNM2), transcript variant 3, mRNA [NM_199077]
870	A_33_P3227492	2,550	up		chromosome 1 open reading frame 148 [Source:HGNC Symbol;Acc:32062] [ENST00000366713]
871	A_33_P3275315	2,550	up		chromosome 10 open reading frame 31 [Source:HGNC Symbol;Acc:23515] [ENST00000379256]
872	A_33_P3378702	2,550	up		Homo sapiens cDNA FLJ45887 fis, clone OCBBF3021502, [AK127786]
873	A_23_P23292	2,550	up	RXRG	Homo sapiens retinoid X receptor, gamma (RXRG), transcript variant 1, mRNA [NM_006917]
874	A_33_P3316318	2,547	up	CEP120	centrosomal protein 120kDa [Source:HGNC Symbol;Acc:26690] [ENST00000395431]
875	A_24_P359671	2,546	up	NTNG1	netrin G1 [Source:HGNC Symbol;Acc:23319] [ENST00000294649]
876	A_33_P3232861	2,545	up		Q3RU97_RALME (Q3RU97) Sulfate transporter/antisigma-factor antagonist STAS:Sulphate transporter, partial (3%) [THC2519244]
877	A_33_P3338382	2,545	up	OR1K1	Homo sapiens olfactory receptor, family 1, subfamily K, member 1 (OR1K1), mRNA [NM_080859]
878	A_33_P3399045	2,545	up		Homo sapiens cDNA clone IMAGE:5242641, [BC032569]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
879	A_23_P171132	2,545	up	EDA2R	Homo sapiens ectodysplasin A2 receptor (EDA2R), transcript variant 2, mRNA [NM_021783]
880	A_23_P216622	2,545	up	FKTN	Homo sapiens fukutin (FKTN), transcript variant 1, mRNA [NM_001079802]
881	A_33_P3335915	2,543	up	SYNE1	Homo sapiens mRNA; cDNA DKFZp547N107 (from clone DKFZp547N107), [AL713682]
882	A_33_P3365710	2,543	up	ATP6V0D1	Homo sapiens cDNA FLJ43534 fis, clone PLACE7001936, [AK125522]
883	A_23_P312874	2,543	up	SPATS1	Homo sapiens spermatogenesis associated, serine-rich 1 (SPATS1), mRNA [NM_145026]
884	A_33_P3417547	2,542	up		
885	A_33_P3380529	2,540	up	PRTFDC1	Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), mRNA [NM_020200]
886	A_33_P3280974	2,539	up		
887	A_33_P3253179	2,539	up		
888	A_32_P46594	2,539	up	LOC145837	Homo sapiens hypothetical LOC145837 (LOC145837), non-coding RNA [NR_026979]
889	A_33_P3210762	2,538	up	ADAMTS7	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 7 (ADAMTS7), mRNA [NM_014272]
890	A_23_P68436	2,536	up	WFDC12	Homo sapiens WAP four-disulfide core domain 12 (WFDC12), mRNA [NM_080869]
891	A_33_P3420976	2,536	up	FAM159B	Homo sapiens family with sequence similarity 159, member B (FAM159B), mRNA [NM_001164442]
892	A_23_P163195	2,535	up	LRFN5	Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA [NM_152447]
893	A_33_P3250343	2,535	up	LOC100133161	Homo sapiens hypothetical LOC100133161 (LOC100133161), non-coding RNA [NR_028326]
894	A_24_P124558	2,535	up	HOXC8	Homo sapiens homeobox C8 (HOXC8), mRNA [NM_022658]
895	A_24_P11900	2,534	up	MYH15	Homo sapiens myosin, heavy chain 15 (MYH15), mRNA [NM_014981]
896	A_33_P3415668	2,534	up	LOC643923	Homo sapiens hypothetical LOC643923 (LOC643923), non-coding RNA [NR_028328]
897	A_32_P125771	2,534	up	RGS22	Homo sapiens regulator of G-protein signaling 22 (RGS22), mRNA [NM_015668]
898	A_33_P3241782	2,532	up	ADD2	Homo sapiens adducin 2 (beta) (ADD2), transcript variant 1, mRNA [NM_001617]
899	A_24_P273180	2,531	up		preferentially expressed antigen in melanoma-like [Source:HGNC Symbol;Acc:34302] [ENST00000337471]
900	A_33_P3677814	2,531	up	NPSA	Homo sapiens prostate-specific antigen mRNA, complete cds, [AF527974]
901	A_23_P167298	2,529	up	C4orf17	Homo sapiens chromosome 4 open reading frame 17 (C4orf17), mRNA [NM_032149]
902	A_33_P3382849	2,528	up	ACR	Homo sapiens acrosin (ACR), mRNA [NM_001097]
903	A_33_P3273737	2,527	up	LOC100129449	Homo sapiens clone FLB7723 PRO2055 mRNA, complete cds, [AF130063]
904	A_33_P3383205	2,526	up	OK/SW-CL,58	Homo sapiens mRNA for OK/SW-CL,58, complete cds, [AB064667]
905	A_33_P3382595	2,525	up	RN7SK	Homo sapiens RNA, 7SK small nuclear (RN7SK), small nuclear RNA [NR_001445]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
906	A_33_P3416966	2,525	up	C6orf168	Homo sapiens chromosome 6 open reading frame 168 (C6orf168), mRNA [NM_032511]
907	A_33_P3387095	2,525	up		
908	A_23_P13271	2,523	up		GB
909	A_33_P3398946	2,522	up	IRF2BP1	Homo sapiens interferon regulatory factor 2 binding protein 1 (IRF2BP1), mRNA [NM_015649]
910	A_33_P3324814	2,522	up		
911	A_33_P3291118	2,521	up	LRRC37B	Homo sapiens leucine rich repeat containing 37B (LRRC37B), mRNA [NM_052888]
912	A_33_P3244007	2,520	up	NEBL	nebulette [Source:HGNC Symbol;Acc:16932] [ENST00000377119]
913	A_32_P178758	2,520	up	LY86-AS1	Homo sapiens LY86 antisense RNA 1 (non-protein coding) (LY86-AS1), non-coding RNA [NR_026970]
914	A_23_P148600	2,520	up	INE1	Homo sapiens inactivation escape 1 (non-protein coding) (INE1), non-coding RNA [NR_024616]
915	A_33_P3313710	2,520	up	LOC100130255	PREDICTED: Homo sapiens hypothetical protein LOC100130255 (LOC100130255), mRNA [XM_001721023]
916	A_33_P3369441	2,520	up	LOC100132111	Homo sapiens hypothetical LOC100132111 (LOC100132111), non-coding RNA [NR_024237]
917	A_33_P3339611	2,519	up		
918	A_23_P7957	2,519	up	GNMT	Homo sapiens glycine N-methyltransferase (GNMT), mRNA [NM_018960]
919	A_23_P207174	2,518	up	GH2	Homo sapiens growth hormone 2 (GH2), transcript variant 2, mRNA [NM_022557]
920	A_33_P3395442	2,517	up	LOC678655	Homo sapiens hypothetical locus LOC678655 (LOC678655), non-coding RNA [NR_015382]
921	A_33_P3286357	2,517	up		
922	A_33_P3314623	2,516	up		GB
923	A_33_P3420011	2,516	up		
924	A_33_P3244433	2,516	up	FAM188B	Homo sapiens cDNA FLJ33507 fis, clone BRAMY2005064, [AK090826]
925	A_33_P3291097	2,514	up	BCAM	Homo sapiens basal cell adhesion molecule (Lutheran blood group) (BCAM), transcript variant 2, mRNA [NM_001013257]
926	A_33_P3415828	2,513	up		Synthetic construct Homo sapiens gateway clone IMAGE:100016753 3' read PLA2G12A mRNA, [CU677870]
927	A_32_P225659	2,513	up	UTS2D	Homo sapiens urotensin 2 domain containing (UTS2D), mRNA [NM_198152]
928	A_33_P3270084	2,511	up		CDC2L1S13 PITSLRE protein kinase alpha SV9 isoform {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (38%) [THC2524986]
929	A_24_P102315	2,511	up	KIAA1755	Homo sapiens KIAA1755 (KIAA1755), mRNA [NM_001029864]
930	A_23_P99386	2,510	up	TNFSF11	Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 1, mRNA [NM_003701]
931	A_33_P3389336	2,510	up		
932	A_33_P3371154	2,509	up	ZNF365	Homo sapiens zinc finger protein 365 (ZNF365), transcript variant C, mRNA [NM_199451]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
933	A_23_P252023	2,508	up	SSX2	Homo sapiens synovial sarcoma, X breakpoint 2 (SSX2), transcript variant 2, mRNA [NM_175698]
934	A_33_P3251518	2,508	up	PYCR2	pyrroline-5-carboxylate reductase family, member 2 [Source:HGNC Symbol;Acc:30262] [ENST00000366823]
935	A_33_P3250333	2,508	up	DNAH10	Homo sapiens dynein, axonemal, heavy chain 10 (DNAH10), mRNA [NM_207437]
936	A_33_P3372600	2,508	up	LOC100129119	PREDICTED: Homo sapiens hypothetical LOC100129119, transcript variant 1 (LOC100129119), partial miscRNA [XR_109159]
937	A_33_P3340065	2,508	up		
938	A_23_P23037	2,507	up	GJA8	Homo sapiens gap junction protein, alpha 8, 50kDa (GJA8), mRNA [NM_005267]
939	A_23_P302060	2,507	up	IFNE	Homo sapiens interferon, epsilon (IFNE), mRNA [NM_176891]
940	A_33_P3485760	2,507	up	EIF3A	eukaryotic translation initiation factor 3, subunit A [Source:HGNC Symbol;Acc:3271] [ENST00000462527]
941	A_33_P3284715	2,507	up	SCARNA7	Homo sapiens small Cajal body-specific RNA 7 (SCARNA7), guide RNA [NR_003001]
942	A_33_P3398965	2,506	up	CALML4	Homo sapiens calmodulin-like 4 (CALML4), transcript variant 1, mRNA [NM_033429]
943	A_33_P3422947	2,505	up	DNAH6	Homo sapiens dynein, axonemal, heavy chain 6 (DNAH6), mRNA [NM_001370]
944	A_24_P320103	2,504	up	MECOM	Homo sapiens MDS1 and EVI1 complex locus (MECOM), transcript variant 4, mRNA [NM_004991]
945	A_23_P160438	2,504	up	MYOG	Homo sapiens myogenin (myogenic factor 4) (MYOG), mRNA [NM_002479]
946	A_23_P73150	2,502	up	TTC25	Homo sapiens tetratricopeptide repeat domain 25 (TTC25), mRNA [NM_031421]
947	A_23_P208240	2,501	up	ZNF160	zinc finger protein 160 [Source:HGNC Symbol;Acc:12948] [ENST00000355147]
948	A_33_P3372199	2,501	up		
949	A_33_P3341821	2,501	up	FAM151A	Homo sapiens family with sequence similarity 151, member A (FAM151A), mRNA [NM_176782]
950	A_33_P3418294	2,501	up	DNAH14	Homo sapiens dynein, axonemal, heavy chain 14 (DNAH14), transcript variant 1, mRNA [NM_001373]
951	A_33_P3325497	2,499	up	FIBIN	Homo sapiens fin bud initiation factor homolog (zebrafish) (FIBIN), mRNA [NM_203371]
952	A_24_P358084	2,498	up		NPIP-like protein LOC729978 [Source:UniProtKB/Swiss-Prot;Acc:A6NJ64] [ENST00000532936]
953	A_24_P319647	2,498	up	FCRL2	Homo sapiens Fc receptor-like 2 (FCRL2), mRNA [NM_030764]
954	A_23_P129367	2,497	up	CCDC135	Homo sapiens coiled-coil domain containing 135 (CCDC135), mRNA [NM_032269]
955	A_33_P3323641	2,497	up		
956	A_32_P14582	2,497	up	C3P1	Homo sapiens complement component 3 precursor pseudogene (C3P1), non-coding RNA [NR_027300]
957	A_33_P3232173	2,496	up	PSPC1	paraspeckle component 1 [Source:HGNC Symbol;Acc:20320] [ENST00000338910]
958	A_33_P3222109	2,494	up	XG	Homo sapiens Xg blood group (XG), transcript variant 2, mRNA [NM_001141919]
959	A_33_P3264910	2,494	up	NKX6-2	Homo sapiens NK6 homeobox 2 (NKX6-2), mRNA [NM_177400]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
960	A_33_P3888568	2,494	up	SNORA70B	UI-H-DT0-aub-m-04-0-UI,s1 NCI_CGAP_DT0 Homo sapiens cDNA clone IMAGE:5867307 3', mRNA sequence [BQ029156]
961	A_23_P346953	2,494	up	DGKB	Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 2, mRNA [NM_145695]
962	A_33_P3223182	2,493	up	TPTE2P3	Homo sapiens transmembrane phosphoinositide 3-phosphatase and tensin homolog 2 pseudogene 3 (TPTE2P3), non-coding RNA [NR_002793]
963	A_33_P3229678	2,492	up	LOC100510659	PREDICTED: Homo sapiens hypothetical protein LOC100510659 (LOC100510659), mRNA [XM_003120642]
964	A_33_P3281003	2,491	up		Homo sapiens cDNA FLJ45587 fis, clone BRTHA3014105, [AK127494]
965	A_33_P3423530	2,491	up	TPK1	thiamin pyrophosphokinase 1 [Source:HGNC Symbol;Acc:17358] [ENST00000549981]
966	A_24_P921327	2,490	up	TAPT1	transmembrane anterior posterior transformation 1 [Source:HGNC Symbol;Acc:26887] [ENST00000505317]
967	A_33_P3225046	2,489	up	CD34	Homo sapiens CD34 molecule (CD34), transcript variant 1, mRNA [NM_001025109]
968	A_33_P3270489	2,489	up	C6orf97	Homo sapiens chromosome 6 open reading frame 97 (C6orf97), mRNA [NM_025059]
969	A_23_P166993	2,488	up	EPHB1	Homo sapiens EPH receptor B1 (EPHB1), mRNA [NM_004441]
970	A_23_P91283	2,488	up	CASS4	Homo sapiens Cas scaffolding protein family member 4 (CASS4), transcript variant 2, mRNA [NM_020356]
971	A_33_P3309670	2,488	up	KIAA1211	Homo sapiens KIAA1211 (KIAA1211), mRNA [NM_020722]
972	A_23_P4096	2,487	up	CA4	Homo sapiens carbonic anhydrase IV (CA4), mRNA [NM_000717]
973	A_33_P3340782	2,485	up	SPINK5	Homo sapiens serine peptidase inhibitor, Kazal type 5 (SPINK5), transcript variant 3, mRNA [NM_001127699]
974	A_23_P93658	2,485	up	ACCN3	Homo sapiens amiloride-sensitive cation channel 3 (ACCN3), transcript variant 3, mRNA [NM_020322]
975	A_33_P3398727	2,484	up		Homo sapiens cDNA clone IMAGE:5270501, [BC041856]
976	A_33_P3353979	2,484	up	SYT15	Homo sapiens synaptotagmin XV (SYT15), transcript variant b, mRNA [NM_181519]
977	A_24_P399230	2,483	up	WFIKKN2	Homo sapiens WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (WFIKKN2), mRNA [NM_175575]
978	A_24_P136124	2,483	up		PREDICTED: Homo sapiens hypothetical protein LOC100505579 (LOC100505579), mRNA [XM_003118806]
979	A_33_P3411372	2,483	up		
980	A_23_P95231	2,482	up	CASC1	Homo sapiens cancer susceptibility candidate 1 (CASC1), transcript variant 1, mRNA [NM_018272]
981	A_33_P3373119	2,481	up		
982	A_33_P3332337	2,481	up	FOLH1	Homo sapiens folate hydrolase (prostate-specific membrane antigen) 1 (FOLH1), transcript variant 4, mRNA [NM_001193472]
983	A_23_P110412	2,478	up	TMEM150C	Homo sapiens transmembrane protein 150C (TMEM150C), mRNA [NM_001080506]
984	A_23_P63972	2,477	up		double C2-like domains, gamma, pseudogene [Source:HGNC Symbol;Acc:37962] [ENST00000495263]
985	A_24_P929388	2,477	up	TMEM169	Homo sapiens transmembrane protein 169 (TMEM169), transcript variant 3, mRNA [NM_138390]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
986	A_33_P3244728	2,477	up	LRP2	Homo sapiens low density lipoprotein receptor-related protein 2 (LRP2), mRNA [NM_004525]
987	A_32_P377008	2,476	up		Q4KGN0_PSEF5 (Q4KGN0) Bll7817, partial (5%) [THC2643762]
988	ERCC-00012_90	2,472	up		Unknown
989	A_33_P3267731	2,472	up	LOC100130954	Homo sapiens hypothetical LOC100130954 (LOC100130954), non-coding RNA [NR_034016]
990	A_23_P6818	2,468	up	SEMA3G	Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G (SEMA3G), mRNA [NM_020163]
991	A_24_P346725	2,468	up		Homo sapiens cDNA FLJ10232 fis, clone HEMBB1000244, [AK001094]
992	A_33_P3240972	2,468	up	LOC100134285	PREDICTED: Homo sapiens hypothetical protein LOC100134285 (LOC100134285), mRNA [XM_003119593]
993	A_23_P133153	2,467	up	DMP1	Homo sapiens dentin matrix acidic phosphoprotein 1 (DMP1), transcript variant 1, mRNA [NM_004407]
994	A_23_P164042	2,467	up	ERN1	Homo sapiens endoplasmic reticulum to nucleus signaling 1 (ERN1), mRNA [NM_001433]
995	A_23_P309720	2,467	up	GABRD	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, delta (GABRD), mRNA [NM_000815]
996	A_33_P3370875	2,466	up		
997	A_33_P3416583	2,465	up	ARAP1	Homo sapiens ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1 (ARAP1), transcript variant 4, mRNA [NM_001135190]
998	A_32_P149546	2,465	up	CROCC	Homo sapiens ciliary rootlet coiled-coil, rootletin (CROCC), mRNA [NM_014675]
999	A_33_P3315715	2,463	up	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2 [Source:HGNC Symbol;Acc:30506] [ENST00000405223]
1000	A_24_P24444	2,463	up	EXOG	Homo sapiens endo/exonuclease (5'-3'), endonuclease G-like (EXOG), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_005107]
1001	A_23_P43412	2,462	up	HEMGN	Homo sapiens hemogen (HEMGN), transcript variant 1, mRNA [NM_018437]
1002	A_23_P252388	2,462	up	SPEF2	Homo sapiens sperm flagellar 2 (SPEF2), transcript variant 1, mRNA [NM_024867]
1003	A_23_P210445	2,461	up	L3MBTL1	Homo sapiens l(3)mbt-like 1 (Drosophila) (L3MBTL1), transcript variant II, mRNA [NM_032107]
1004	A_23_P148829	2,461	up	ACTRT2	Homo sapiens actin-related protein T2 (ACTRT2), mRNA [NM_080431]
1005	A_33_P3209816	2,461	up	DPY19L3	Homo sapiens dpy-19-like 3 (C, elegans) (DPY19L3), transcript variant 1, mRNA [NM_207325]
1006	A_24_P332816	2,461	up	RIMS2	Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), transcript variant 2, mRNA [NM_014677]
1007	A_33_P3374365	2,460	up	LOC100129702	PREDICTED: Homo sapiens hypothetical protein LOC100129702 (LOC100129702), mRNA [XM_001714010]
1008	A_23_P98070	2,460	up	PDE6C	Homo sapiens phosphodiesterase 6C, cGMP-specific, cone, alpha prime (PDE6C), mRNA [NM_006204]
1009	A_33_P3376493	2,460	up	AGTR2	Homo sapiens angiotensin II receptor, type 2 (AGTR2), mRNA [NM_000686]
1010	A_33_P3281563	2,459	up		
1011	A_33_P3335366	2,459	up	MAML3	Homo sapiens mastermind-like 3 (Drosophila) (MAML3), mRNA [NM_018717]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1012	A_33_P3216621	2,459	up		
1013	A_33_P3358893	2,458	up	PRM2	Homo sapiens protamine 2 (PRM2), mRNA [NM_002762]
1014	A_33_P3293254	2,457	up	GPSM1	Homo sapiens G-protein signaling modulator 1 (GPSM1), transcript variant 2, mRNA [NM_015597]
1015	A_23_P54612	2,457	up	DNAAF1	Homo sapiens dynein, axonemal, assembly factor 1 (DNAAF1), mRNA [NM_178452]
1016	A_33_P3328653	2,456	up	CELSR1	Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA [NM_014246]
1017	A_23_P164405	2,456	up	KRTAP2-4	Homo sapiens keratin associated protein 2-4 (KRTAP2-4), mRNA [NM_033184]
1018	A_33_P3399228	2,456	up	LINGO1	Homo sapiens leucine rich repeat and Ig domain containing 1 (LINGO1), mRNA [NM_032808]
1019	A_24_P307724	2,455	up	FLJ33360	Homo sapiens FLJ33360 protein (FLJ33360), non-coding RNA [NR_028351]
1020	A_33_P3345608	2,455	up	C10orf137	Homo sapiens chromosome 10 open reading frame 137 (C10orf137), transcript variant 1, mRNA [NM_001202438]
1021	A_33_P3503937	2,455	up	LOC284581	Homo sapiens cDNA FLJ37107 fis, clone BRACE2020157, [AK094426]
1022	A_23_P401774	2,453	up	ELMOD1	Homo sapiens ELMO/CED-12 domain containing 1 (ELMOD1), transcript variant 1, mRNA [NM_018712]
1023	A_33_P3289167	2,453	up	ZBTB32	Homo sapiens zinc finger and BTB domain containing 32 (ZBTB32), mRNA [NM_014383]
1024	A_32_P65706	2,453	up		chromosome 9 open reading frame 92 [Source:HGNC Symbol;Acc:19054] [ENST00000380683]
1025	A_33_P3322519	2,452	up	VWA5B2	Homo sapiens von Willebrand factor A domain containing 5B2 (VWA5B2), mRNA [NM_138345]
1026	A_23_P37410	2,451	up	CYP19A1	Homo sapiens cytochrome P450, family 19, subfamily A, polypeptide 1 (CYP19A1), transcript variant 2, mRNA [NM_031226]
1027	A_33_P3236177	2,450	up	ANG	Homo sapiens angiogenin, ribonuclease, RNase A family, 5 (ANG), transcript variant 1, mRNA [NM_001145]
1028	A_23_P12241	2,450	up	MCOLN3	Homo sapiens mucolipin 3 (MCOLN3), mRNA [NM_018298]
1029	A_24_P796321	2,449	up	LEUTX	Homo sapiens leucine twenty homeobox (LEUTX), mRNA [NM_001143832]
1030	A_23_P430718	2,448	up	SPATA19	Homo sapiens spermatogenesis associated 19 (SPATA19), mRNA [NM_174927]
1031	A_33_P3232655	2,448	up	GHRHR	Homo sapiens growth hormone releasing hormone receptor (GHRHR), mRNA [NM_000823]
1032	A_23_P42882	2,448	up	CAMK2B	Homo sapiens calcium/calmodulin-dependent protein kinase II beta (CAMK2B), transcript variant 6, mRNA [NM_172082]
1033	A_23_P143857	2,446	up	LRRC3B	Homo sapiens leucine rich repeat containing 3B (LRRC3B), mRNA [NM_052953]
1034	A_33_P3381292	2,445	up		
1035	A_33_P3321120	2,445	up		
1036	A_23_P143902	2,444	up	P2RY12	Homo sapiens purinergic receptor P2Y, G-protein coupled, 12 (P2RY12), transcript variant 1, mRNA [NM_022788]
1037	A_33_P3330911	2,444	up	BCAS1	Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), mRNA [NM_003657]
1038	A_33_P3261197	2,444	up	NCBP1	Homo sapiens nuclear cap binding protein subunit 1, 80kDa (NCBP1), mRNA [NM_002486]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1039	A_23_P343963	2,443	up	FAM83F	Homo sapiens family with sequence similarity 83, member F (FAM83F), mRNA [NM_138435]
1040	A_33_P3305973	2,443	up		
1041	A_33_P3278813	2,443	up	LOC100127885	PREDICTED: Homo sapiens hypothetical protein LOC100127885 (LOC100127885), mRNA [XM_001721771]
1042	A_23_P300847	2,443	up	DIO3OS	Homo sapiens clone 6 DIO3AS mRNA, partial sequence; alternatively spliced, [AF469204]
1043	A_33_P3262799	2,442	up	ZNF280D	zinc finger protein 280D [Source:HGNC Symbol;Acc:25953] [ENST00000396245]
1044	A_33_P3346157	2,442	up	TMED8	Homo sapiens transmembrane emp24 protein transport domain containing 8 (TMED8), mRNA [NM_213601]
1045	A_23_P401709	2,442	up	C20orf196	Homo sapiens chromosome 20 open reading frame 196 (C20orf196), mRNA [NM_152504]
1046	A_24_P112377	2,441	up	DDX31	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA [NM_138620]
1047	A_33_P3356816	2,441	up	LCE1B	Homo sapiens late cornified envelope 1B (LCE1B), mRNA [NM_178349]
1048	A_33_P3394213	2,440	up	GRIN3B	Homo sapiens glutamate receptor, ionotropic, N-methyl-D-aspartate 3B (GRIN3B), mRNA [NM_138690]
1049	A_33_P3285145	2,440	up	LOC100131826	PREDICTED: Homo sapiens TSSP3028 (LOC100131826), miscRNA [XR_109830]
1050	A_33_P3365441	2,440	up	LHX9	LIM homeobox 9 [Source:HGNC Symbol;Acc:14222] [ENST00000367388]
1051	A_23_P159406	2,439	up	SPRR1B	Homo sapiens small proline-rich protein 1B (SPRR1B), mRNA [NM_003125]
1052	A_24_P366859	2,438	up	USHBP1	Homo sapiens Usher syndrome 1C binding protein 1 (USHBP1), mRNA [NM_031941]
1053	A_33_P3773200	2,438	up	LOC285766	Homo sapiens cDNA FLJ40227 fis, clone TESTI2022462, [AK097546]
1054	A_32_P327679	2,437	up	DKFZP434K028	Homo sapiens hypothetical LOC26070 (DKFZP434K028), non-coding RNA [NR_026882]
1055	A_33_P3330944	2,437	up		
1056	A_33_P3355266	2,437	up	TINAGL1	Homo sapiens tubulointerstitial nephritis antigen-like 1 (TINAGL1), transcript variant 1, mRNA [NM_022164]
1057	A_33_P3236993	2,436	up	ARVCF	Homo sapiens armadillo repeat gene deleted in velocardiofacial syndrome (ARVCF), mRNA [NM_001670]
1058	A_33_P3230798	2,436	up	MUSK	muscle, skeletal, receptor tyrosine kinase [Source:HGNC Symbol;Acc:7525] [ENST00000374441]
1059	A_33_P3299140	2,435	up	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa [Source:HGNC Symbol;Acc:4668] [ENST00000372089]
1060	A_23_P326931	2,435	up	TTC18	Homo sapiens tetratricopeptide repeat domain 18 (TTC18), mRNA [NM_145170]
1061	A_33_P3347057	2,435	up	LOC100132005	Homo sapiens cDNA FLJ35343 fis, clone PROST2015932, [AK092662]
1062	A_33_P3387786	2,435	up		
1063	A_33_P3294985	2,435	up	JPX	Homo sapiens JPX transcript, XIST activator (non-protein coding) (JPX), non-coding RNA [NR_024582]
1064	A_33_P3338539	2,434	up		
1065	A_23_P350698	2,434	up	ANKFN1	Homo sapiens ankyrin-repeat and fibronectin type III domain containing 1 (ANKFN1), mRNA [NM_153228]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1066	A_33_P3286916	2,433	up	PDZD7	Homo sapiens PDZ domain containing 7 (PDZD7), transcript variant 1, mRNA [NM_001195263]
1067	A_33_P3383075	2,432	up		
1068	A_33_P3283525	2,429	up	ENAH	enabled homolog (Drosophila) [Source:HGNC Symbol;Acc:18271] [ENST00000498108]
1069	A_24_P292470	2,428	up	UCP3	Homo sapiens uncoupling protein 3 (mitochondrial, proton carrier) (UCP3), nuclear gene encoding mitochondrial protein, transcript variant short, mRNA [NM_022803]
1070	A_23_P216845	2,428	up	GFI1B	Homo sapiens growth factor independent 1B transcription repressor (GFI1B), transcript variant 1, mRNA [NM_004188]
1071	A_33_P3245699	2,428	up		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E9PF64] [ENST00000318959]
1072	A_33_P3341490	2,428	up	KRT42P	Homo sapiens keratin 42 pseudogene (KRT42P), non-coding RNA [NR_033415]
1073	A_33_P3409849	2,427	up		chromosome 12 open reading frame 63 [Source:HGNC Symbol;Acc:24777] [ENST00000342887]
1074	A_33_P3379956	2,427	up	DCDC1	doublecortin domain containing 1 [Source:HGNC Symbol;Acc:20625] [ENST00000342355]
1075	A_33_P3272395	2,427	up	RAB19	Homo sapiens RAB19, member RAS oncogene family (RAB19), mRNA [NM_001008749]
1076	A_33_P3298092	2,427	up	LOC100131756	Homo sapiens cDNA FLJ38820 fis, clone LIVER2008473, [AK096139]
1077	A_33_P3381117	2,426	up	LOC100128563	PREDICTED: Homo sapiens hypothetical protein LOC100128563 (LOC100128563), mRNA [XM_003118860]
1078	A_33_P3424872	2,426	up		RST11351 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG192243]
1079	A_23_P433798	2,425	up	PODNL1	Homo sapiens podocan-like 1 (PODNL1), transcript variant 1, mRNA [NM_024825]
1080	A_33_P3771067	2,424	up	LOC283140	Homo sapiens cDNA FLJ37956 fis, clone CTONG2009527, [AK095275]
1081	A_24_P589855	2,424	up		Q7SYZ0_XENLA (Q7SYZ0) Vrk1-prov protein, partial (8%) [THC2662209]
1082	A_33_P3332248	2,424	up	ADRA1A	adrenergic, alpha-1A-, receptor [Source:HGNC Symbol;Acc:277] [ENST00000380573]
1083	A_33_P3240951	2,423	up	DPF3	Homo sapiens D4, zinc and double PHD fingers, family 3 (DPF3), mRNA [NM_012074]
1084	A_33_P3268649	2,423	up	SLC2A11	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 11 (SLC2A11), transcript variant 1, mRNA [NM_030807]
1085	A_33_P3213119	2,422	up	HAS2-AS1	Homo sapiens HAS2 antisense RNA 1 (non-protein coding) (HAS2-AS1), antisense RNA [NR_002835]
1086	A_33_P3233219	2,422	up	NPBWR1	Homo sapiens neuropeptides B/W receptor 1 (NPBWR1), mRNA [NM_005285]
1087	A_33_P3310415	2,422	up		PREDICTED: Homo sapiens hypothetical protein LOC100506601 (LOC100506601), mRNA [XM_003118559]
1088	A_33_P3365760	2,422	up	STAP1	Homo sapiens signal transducing adaptor family member 1 (STAP1), mRNA [NM_012108]
1089	A_33_P3363341	2,422	up	TMEM212	Homo sapiens transmembrane protein 212 (TMEM212), mRNA [NM_001164436]
1090	A_33_P3854953	2,421	up	LOC440117	Homo sapiens hypothetical LOC440117 (LOC440117), non-coding RNA [NR_033970]
1091	A_33_P3340129	2,420	up	LOC100128551	Homo sapiens cDNA FLJ43158 fis, clone ERLTF2000324, [AK125148]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1092	A_33_P3323218	2,418	up	ALS2CR8	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8 (ALS2CR8), mRNA [NM_024744]
1093	A_33_P3377911	2,418	up		
1094	A_24_P131236	2,418	up	SV2A	Homo sapiens synaptic vesicle glycoprotein 2A (SV2A), mRNA [NM_014849]
1095	A_33_P3339625	2,416	up	IL17C	Homo sapiens interleukin 17C (IL17C), mRNA [NM_013278]
1096	A_33_P3228773	2,416	up	CYYR1	cysteine/tyrosine-rich 1 [Source:HGNC Symbol;Acc:16274] [ENST00000400043]
1097	A_24_P160680	2,416	up	CCDC40	Homo sapiens coiled-coil domain containing 40 (CCDC40), mRNA [NM_017950]
1098	A_33_P3270354	2,415	up		
1099	A_33_P3414022	2,414	up		
1100	A_23_P82379	2,413	up	CACNA2D1	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA [NM_000722]
1101	A_23_P35055	2,413	up	NPHS2	Homo sapiens nephrosis 2, idiopathic, steroid-resistant (podocin) (NPHS2), mRNA [NM_014625]
1102	A_33_P3358322	2,413	up	LOC338667	Homo sapiens full length insert cDNA clone ZD42A08, [AF086259]
1103	A_33_P3422951	2,413	up	DNAH6	dynein, axonemal, heavy chain 6 [Source:HGNC Symbol;Acc:2951] [ENST00000398278]
1104	A_33_P3408683	2,412	up		
1105	A_33_P3234764	2,412	up		PREDICTED: Homo sapiens hypothetical protein LOC100505631 (LOC100505631), mRNA [XM_003119155]
1106	A_33_P3337405	2,412	up	LOC440993	PREDICTED: Homo sapiens hypothetical LOC440993 (LOC440993), miscRNA [XR_110395]
1107	A_33_P3288079	2,411	up		
1108	A_33_P3249081	2,410	up	FSTL4	Homo sapiens follistatin-like 4 (FSTL4), mRNA [NM_015082]
1109	A_23_P259707	2,410	up	LPPR1	Homo sapiens lipid phosphate phosphatase-related protein type 1 (LPPR1), transcript variant 1, mRNA [NM_207299]
1110	A_33_P3380086	2,410	up	PXN	paxillin [Source:HGNC Symbol;Acc:9718] [ENST00000323871]
1111	A_23_P81158	2,410	up	ADH1C	Homo sapiens alcohol dehydrogenase 1C (class I), gamma polypeptide (ADH1C), mRNA [NM_000669]
1112	A_33_P3222761	2,409	up		T cell receptor alpha variable 9-1 [Source:HGNC Symbol;Acc:12153] [ENST00000390431]
1113	A_33_P3257891	2,409	up	GSTA3	Homo sapiens glutathione S-transferase alpha 3 (GSTA3), mRNA [NM_000847]
1114	A_23_P127781	2,408	up	SCGB1D1	Homo sapiens secretoglobin, family 1D, member 1 (SCGB1D1), mRNA [NM_006552]
1115	A_33_P3359743	2,408	up		Q2H4V1_CHAGB (Q2H4V1) Predicted protein, partial (4%) [THC2773215]
1116	A_23_P2283	2,407	up	TAC3	Homo sapiens tachykinin 3 (TAC3), transcript variant 1, mRNA [NM_013251]
1117	A_23_P396917	2,406	up	C11orf63	Homo sapiens chromosome 11 open reading frame 63 (C11orf63), transcript variant 2, mRNA [NM_199124]
1118	A_33_P3302290	2,406	up	AACSP1	Homo sapiens acetoacetyl-CoA synthetase pseudogene 1 (AACSP1), non-coding RNA [NR_024035]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1119	A_33_P3266195	2,404	up	LOC402382	PREDICTED: Homo sapiens hypothetical protein LOC402382 (LOC402382), mRNA [XM_378090]
1120	A_33_P3272849	2,404	up	LCN8	lipocalin 8 [Source:HGNC Symbol;Acc:27038] [ENST00000479767]
1121	A_33_P3302861	2,402	up	RPGRIP1L	Homo sapiens RPGRIP1-like (RPGRIP1L), transcript variant 1, mRNA [NM_015272]
1122	A_33_P3333890	2,402	up	LCORL	Homo sapiens ligand dependent nuclear receptor corepressor-like (LCORL), transcript variant 1, mRNA [NM_001166139]
1123	A_33_P3346083	2,402	up	DCDC1	Homo sapiens doublecortin domain containing 1 (DCDC1), mRNA [NM_181807]
1124	A_24_P116606	2,402	up	WWOX	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 2, mRNA [NM_130791]
1125	A_33_P3209497	2,401	up		GB
1126	A_33_P3552465	2,400	up	ZNF852	zinc finger protein 852 [Source:HGNC Symbol;Acc:27713] [ENST00000463067]
1127	A_23_P93704	2,399	up	C7orf61	Homo sapiens chromosome 7 open reading frame 61 (C7orf61), mRNA [NM_001004323]
1128	A_33_P3323904	2,397	up	WTH3DI	Homo sapiens RAB6C-like (WTH3DI), mRNA [NM_001077637]
1129	A_24_P188447	2,396	up	ELAVL4	Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) (ELAVL4), transcript variant 1, mRNA [NM_021952]
1130	A_23_P103011	2,396	up	RAB36	Homo sapiens RAB36, member RAS oncogene family (RAB36), mRNA [NM_004914]
1131	A_33_P3302518	2,396	up	CCDC40	Homo sapiens coiled-coil domain containing 40 (CCDC40), mRNA [NM_017950]
1132	A_23_P320622	2,396	up	TTTY10	Homo sapiens testis-specific transcript, Y-linked 10 (non-protein coding) (TTTY10), non-coding RNA [NR_001542]
1133	A_23_P79015	2,396	up	SCN1B	Homo sapiens sodium channel, voltage-gated, type I, beta (SCN1B), transcript variant b, mRNA [NM_199037]
1134	A_24_P579356	2,395	up	ARHGAP28	Homo sapiens Rho GTPase activating protein 28 (ARHGAP28), mRNA [NM_001010000]
1135	A_33_P3228355	2,394	up	ERV3-1	Homo sapiens endogenous retrovirus group 3, member 1 (ERV3-1), mRNA [NM_001007253]
1136	A_32_P505133	2,393	up	C19orf47	Homo sapiens chromosome 19 open reading frame 47 (C19orf47), mRNA [NM_178830]
1137	A_32_P199429	2,393	up	NCAM2	neural cell adhesion molecule 2 [Source:HGNC Symbol;Acc:7657] [ENST00000400546]
1138	A_33_P3381796	2,393	up	LOC100509073	PREDICTED: Homo sapiens hypothetical protein LOC100509073 (LOC100509073), mRNA [XM_003119065]
1139	A_33_P3251751	2,393	up	CMBL	Homo sapiens carboxymethylenebutenolidase homolog (Pseudomonas) (CMBL), mRNA [NM_138809]
1140	A_32_P71571	2,393	up	FAM19A4	Homo sapiens family with sequence similarity 19 (chemokine (C-C motif)-like), member A4 (FAM19A4), transcript variant 1, mRNA [NM_182522]
1141	A_23_P25176	2,392	up	TBX5	Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA [NM_080718]
1142	A_33_P3410806	2,392	up	CLDN10	Homo sapiens claudin 10 (CLDN10), transcript variant a, mRNA [NM_182848]
1143	A_23_P324605	2,391	up	DNAH6	Homo sapiens dynein, axonemal, heavy chain 6 (DNAH6), mRNA [NM_001370]
1144	A_33_P3405848	2,389	up	TPO	Homo sapiens thyroid peroxidase (TPO), transcript variant 2, mRNA [NM_175719]
1145	A_33_P3422728	2,388	up	CNTNAP3	Homo sapiens contactin associated protein-like 3 (CNTNAP3), mRNA [NM_033655]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1146	A_33_P3311498	2,388	up	LOC283392	Homo sapiens hypothetical LOC283392 (LOC283392), transcript variant 1, non-coding RNA [NR_026837]
1147	A_33_P3365501	2,388	up		
1148	A_33_P3255165	2,387	up		PREDICTED: Homo sapiens hypothetical LOC100132116 (LOC100132116), miscRNA [XR_110433]
1149	A_33_P3250861	2,387	up	ZIC3	Zic family member 3 (odd-paired homolog, Drosophila) [Source:HGNC Symbol;Acc:12874] [ENST00000370606]
1150	A_33_P3420224	2,387	up	ENTPD8	Homo sapiens ectonucleoside triphosphate diphosphohydrolase 8 (ENTPD8), transcript variant 1, mRNA [NM_001033113]
1151	A_23_P115519	2,387	up	LCE3D	Homo sapiens late cornified envelope 3D (LCE3D), mRNA [NM_032563]
1152	A_23_P84995	2,386	up	MTMR8	Homo sapiens myotubularin related protein 8 (MTMR8), mRNA [NM_017677]
1153	A_23_P418431	2,386	up	C6orf164	Homo sapiens chromosome 6 open reading frame 164 (C6orf164), non-coding RNA [NR_026784]
1154	A_33_P3363804	2,384	up	NCAM1	Homo sapiens neural cell adhesion molecule 1 (NCAM1), transcript variant 4, mRNA [NM_001242608]
1155	A_33_P3312301	2,383	up	CIT	Homo sapiens citron (rho-interacting, serine/threonine kinase 21) (CIT), transcript variant 1, mRNA [NM_001206999]
1156	A_33_P3309809	2,383	up	RHBDD1	rhomboid domain containing 1 [Source:HGNC Symbol;Acc:23081] [ENST00000409053]
1157	A_33_P3368034	2,381	up		
1158	A_23_P424561	2,381	up	RHOV	Homo sapiens ras homolog gene family, member V (RHOV), mRNA [NM_133639]
1159	A_23_P334798	2,381	up	LRRC2	Homo sapiens leucine rich repeat containing 2 (LRRC2), mRNA [NM_024512]
1160	A_23_P29057	2,380	up	KCNJ6	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA [NM_002240]
1161	A_33_P3328390	2,379	up		cDNA FLJ34594 fis, clone KIDNE2009109 [Source:UniProtKB/TrEMBL;Acc:Q8NAX6] [ENST00000314040]
1162	A_33_P3246623	2,378	up	CCDC18	Homo sapiens coiled-coil domain containing 18 (CCDC18), mRNA [NM_206886]
1163	A_32_P8221	2,378	up	GRM8	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), transcript variant 1, mRNA [NM_000845]
1164	A_32_P34046	2,376	up	HFM1	Homo sapiens HFM1, ATP-dependent DNA helicase homolog (S, cerevisiae) (HFM1), mRNA [NM_001017975]
1165	A_33_P3273854	2,375	up	NAALADL2	Homo sapiens N-acetylated alpha-linked acidic dipeptidase-like 2 (NAALADL2), mRNA [NM_207015]
1166	A_33_P3302916	2,373	up	BACH2	Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), transcript variant 1, mRNA [NM_021813]
1167	A_33_P3539223	2,372	up	C9orf100	Homo sapiens chromosome 9 open reading frame 100 (C9orf100), mRNA [NM_032818]
1168	A_23_P312752	2,370	up	KCNJ13	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 13 (KCNJ13), transcript variant 1, mRNA [NM_002242]
1169	A_33_P3318357	2,370	up	ALKBH8	Homo sapiens alkB, alkylation repair homolog 8 (E, coli) (ALKBH8), mRNA [NM_138775]
1170	A_33_P3209209	2,370	up		
1171	A_33_P3381378	2,370	up	PAX1	Homo sapiens paired box 1 (PAX1), mRNA [NM_006192]
1172	A_33_P3413759	2,369	up	ACER2	Homo sapiens alkaline ceramidase 2 (ACER2), mRNA [NM_001010887]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1173	A_33_P3423626	2,369	up		PREDICTED: Homo sapiens hypothetical LOC151121 (LOC151121), miscRNA [XR_112384]
1174	A_33_P3282963	2,369	up	TJP2	tight junction protein 2 (zona occludens 2) [Source:HGNC Symbol;Acc:11828] [ENST00000377259]
1175	A_33_P3400302	2,369	up	TTTY18	Homo sapiens testis-specific transcript, Y-linked 18 (non-protein coding) (TTTY18), non-coding RNA [NR_001550]
1176	A_33_P3310548	2,367	up	LOC100131131	PREDICTED: Homo sapiens AHPA9419 (LOC100131131), miscRNA [XR_109928]
1177	A_33_P3291836	2,367	up		
1178	A_23_P214300	2,367	up	GSTA2	Homo sapiens glutathione S-transferase alpha 2 (GSTA2), mRNA [NM_000846]
1179	A_33_P3366301	2,367	up	C14orf23	Homo sapiens chromosome 14 open reading frame 23 (C14orf23), transcript variant 2, non-coding RNA [NR_026732]
1180	A_23_P103765	2,366	up	FCER1A	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A), mRNA [NM_002001]
1181	A_33_P3382229	2,366	up	TNNT3	Homo sapiens troponin T type 3 (skeletal, fast) (TNNT3), transcript variant 1, mRNA [NM_006757]
1182	A_33_P3310159	2,365	up	DGKB	Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA [NM_004080]
1183	A_23_P337270	2,364	up	NEK10	NIMA (never in mitosis gene a)- related kinase 10 [Source:HGNC Symbol;Acc:18592] [ENST00000383770]
1184	A_23_P302470	2,363	up	SULT1B1	Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA [NM_014465]
1185	A_33_P3342752	2,362	up		calpain 8 [Source:HGNC Symbol;Acc:1485] [ENST00000366873]
1186	A_23_P200579	2,362	up	CELA3B	Homo sapiens chymotrypsin-like elastase family, member 3B (CELA3B), mRNA [NM_007352]
1187	A_33_P3415410	2,360	up	PTCH1	Homo sapiens patched 1 (PTCH1), transcript variant 1a, mRNA [NM_001083602]
1188	A_33_P3229672	2,360	up		Q4SEQ2_TETNG (Q4SEQ2) Chromosome 3 SCAF14614, whole genome shotgun sequence, (Fragment), partial (28%) [THC2651904]
1189	A_33_P3414192	2,359	up	SORCS1	Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), transcript variant 6, mRNA [NM_001206572]
1190	A_33_P3318971	2,359	up	METTL20	methyltransferase like 20 [Source:HGNC Symbol;Acc:28739] [ENST00000357721]
1191	A_33_P3326989	2,358	up	RAGE	Homo sapiens renal tumor antigen (RAGE), mRNA [NM_014226]
1192	A_23_P38696	2,358	up	DSC1	Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1b, mRNA [NM_004948]
1193	A_32_P180315	2,357	up	C9orf174	Homo sapiens chromosome 9 open reading frame 174 (C9orf174), mRNA [NM_020893]
1194	A_33_P3238623	2,357	up	LOC729723	Homo sapiens hypothetical LOC729723 (LOC729723), non-coding RNA [NR_034113]
1195	A_24_P334130	2,356	up	FN1	Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA [NM_054034]
1196	DCP_22_9	2,356	up		Unknown
1197	A_23_P46894	2,356	up	CHAT	Homo sapiens choline O-acetyltransferase (CHAT), transcript variant M, mRNA [NM_020549]
1198	A_33_P3409544	2,356	up	HHAT	hedgehog acyltransferase [Source:HGNC Symbol;Acc:18270] [ENST00000391905]
1199	A_24_P393565	2,355	up	ZNF396	zinc finger protein 396 [Source:HGNC Symbol;Acc:18824] [ENST00000399057]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1200	A_33_P3390955	2,355	up	HPVC1	Homo sapiens human papillomavirus (type 18) E5 central sequence-like 1 (HPVC1), non-coding RNA [NR_004422]
1201	A_33_P3227452	2,355	up		PREDICTED: Homo sapiens hypothetical protein LOC100507627 (LOC100507627), mRNA [XM_003118686]
1202	A_24_P874052	2,355	up	LOC100132460	PREDICTED: Homo sapiens hypothetical protein LOC100132460 (LOC100132460), partial mRNA [XM_003119194]
1203	A_32_P160563	2,354	up	OPCML	Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), transcript variant 2, mRNA [NM_001012393]
1204	A_33_P3286352	2,354	up	LOC219347	Homo sapiens hypothetical LOC219347 (LOC219347), transcript variant 1, non-coding RNA [NR_027428]
1205	A_23_P68669	2,352	up	CHODL	Homo sapiens chondrolectin (CHODL), transcript variant 1, mRNA [NM_024944]
1206	A_24_P72646	2,350	up	FLJ14107	Homo sapiens hypothetical LOC80094 (FLJ14107), non-coding RNA [NR_027715]
1207	A_24_P394075	2,350	up	NT5C1B	Homo sapiens 5'-nucleotidase, cytosolic IB (NT5C1B), transcript variant 1, mRNA [NM_001002006]
1208	A_33_P3216083	2,350	up	SHPRH	Homo sapiens SNF2 histone linker PHD RING helicase (SHPRH), transcript variant 2, mRNA [NM_173082]
1209	A_33_P3215729	2,349	up		
1210	A_33_P3219711	2,349	up	SUMF1	sulfatase modifying factor 1 [Source:HGNC Symbol;Acc:20376] [ENST00000534863]
1211	A_33_P3271634	2,349	up	HLA-DPB1	major histocompatibility complex, class II, DP beta 1 [Source:HGNC Symbol;Acc:4940] [ENST00000466949]
1212	A_33_P3306307	2,348	up	KRT26	Homo sapiens keratin 26 (KRT26), mRNA [NM_181539]
1213	A_32_P84242	2,348	up	FAM169A	Homo sapiens family with sequence similarity 169, member A (FAM169A), mRNA [NM_015566]
1214	A_33_P3280157	2,347	up	SNORD116-19	Homo sapiens small nucleolar RNA, C/D box 116-19 (SNORD116-19), small nucleolar RNA [NR_001290]
1215	A_33_P3259560	2,347	up		
1216	A_33_P3349395	2,345	up	CECR2	Homo sapiens CECR2B mRNA, partial cds, [AF411609]
1217	A_33_P3307840	2,345	up	LRRC7	leucine rich repeat containing 7 [Source:HGNC Symbol;Acc:18531] [ENST00000370958]
1218	A_24_P157370	2,344	up	IL17RB	Homo sapiens interleukin 17 receptor B (IL17RB), mRNA [NM_018725]
1219	A_33_P3209581	2,343	up	IQSEC3	Homo sapiens IQ motif and Sec7 domain 3 (IQSEC3), transcript variant 1, mRNA [NM_001170738]
1220	A_23_P87982	2,343	up	ATP12A	Homo sapiens ATPase, H+/K+ transporting, nongastric, alpha polypeptide (ATP12A), transcript variant 2, mRNA [NM_001676]
1221	A_33_P3263359	2,343	up	DGKA	diacylglycerol kinase, alpha 80kDa [Source:HGNC Symbol;Acc:2849] [ENST00000546995]
1222	A_33_P3241090	2,342	up	OR6Q1	Homo sapiens olfactory receptor, family 6, subfamily Q, member 1 (OR6Q1), mRNA [NM_001005186]
1223	A_33_P3423563	2,340	up		
1224	A_33_P3214432	2,339	up	ZC3HAV1L	Homo sapiens zinc finger CCCH-type, antiviral 1-like (ZC3HAV1L), mRNA [NM_080660]
1225	A_33_P3307945	2,338	up		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7EP55] [ENST00000409515]
1226	A_33_P3421144	2,338	up	FLJ39061	PREDICTED: Homo sapiens hypothetical protein FLJ39061 (FLJ39061), miscRNA [XR_108418]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1227	A_33_P3741678	2,338	up	LOC284926	full-length cDNA clone CS0DB004YM09 of Neuroblastoma Cot 10-normalized of Homo sapiens (human), [CR624447]
1228	A_33_P3242965	2,337	up	ATAD3C	Homo sapiens ATPase family, AAA domain containing 3C (ATAD3C), mRNA [NM_001039211]
1229	A_33_P3371215	2,337	up		O02123_CAEEL (O02123) Prion-like-(Q/n-rich)-domain-bearing protein protein 75, isoform a, partial (8%) [THC2784943]
1230	A_33_P3209326	2,337	up	LOC729558	Homo sapiens cDNA FLJ39676 fis, clone SMINT2009832, [AK096995]
1231	A_24_P833129	2,337	up	ISPD	Homo sapiens isoprenoid synthase domain containing (ISPD), transcript variant 1, mRNA [NM_001101426]
1232	A_33_P3261957	2,335	up	CALCRL	Homo sapiens calcitonin receptor-like (CALCRL), mRNA [NM_005795]
1233	A_33_P3423017	2,334	up		
1234	A_33_P3232120	2,333	up	NELF	nasal embryonic LHRH factor [Source:HGNC Symbol;Acc:29843] [ENST00000371468]
1235	A_33_P3412603	2,333	up		Homo sapiens cDNA FLJ43215 fis, clone FEBRA2021908, [AK125205]
1236	A_32_P78681	2,333	up	GLP2R	glucagon-like peptide 2 receptor [Source:HGNC Symbol;Acc:4325] [ENST00000262441]
1237	A_33_P3309734	2,332	up	CCDC108	Homo sapiens coiled-coil domain containing 108 (CCDC108), transcript variant 2, mRNA [NM_152389]
1238	A_23_P50039	2,331	up	MC5R	Homo sapiens melanocortin 5 receptor (MC5R), mRNA [NM_005913]
1239	A_33_P3336053	2,331	up	ANKK1	Homo sapiens ankyrin repeat and kinase domain containing 1 (ANKK1), mRNA [NM_178510]
1240	A_33_P3465703	2,331	up	SNORA60	601888042F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121819 5', mRNA sequence [BF304636]
1241	A_32_P831181	2,326	up	BRI3BP	Homo sapiens BRI3 binding protein (BRI3BP), mRNA [NM_080626]
1242	A_33_P3684897	2,325	up	FLJ30064	DA730659 NT2RM4 Homo sapiens cDNA clone NT2RM4000525 5', mRNA sequence [DA730659]
1243	A_33_P3357738	2,325	up	LOC728196	Homo sapiens cDNA clone IMAGE:4820483, [BC021736]
1244	A_24_P343559	2,325	up	NTRK2	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), transcript variant a, mRNA [NM_006180]
1245	A_23_P351535	2,325	up	DBIL5P	Homo sapiens diazepam binding inhibitor-like 5, pseudogene (DBIL5P), non-coding RNA [NR_024120]
1246	A_23_P432005	2,324	up	C2orf51	Homo sapiens chromosome 2 open reading frame 51 (C2orf51), mRNA [NM_152670]
1247	A_24_P230514	2,324	up	LOC100130924	Homo sapiens cDNA FLJ37105 fis, clone BRACE2019510, [AK094424]
1248	A_23_P140362	2,323	up	VRTN	Homo sapiens vertebrae development homolog (pig) (VRTN), mRNA [NM_018228]
1249	A_24_P187614	2,323	up	LOC100129648	Homo sapiens cDNA FLJ40318 fis, clone TESTI2030556, [AK097637]
1250	A_33_P3381052	2,322	up	OR10K1	Homo sapiens olfactory receptor, family 10, subfamily K, member 1 (OR10K1), mRNA [NM_001004473]
1251	A_33_P3399064	2,321	up	RN5-8S1	Homo sapiens RNA, 5,8S ribosomal 1 (RN5-8S1), ribosomal RNA [NR_003285]
1252	A_24_P659036	2,321	up	FAM116B	Homo sapiens family with sequence similarity 116, member B (FAM116B), mRNA [NM_001001794]
1253	A_23_P160167	2,321	up	TSPAN1	Homo sapiens tetraspanin 1 (TSPAN1), mRNA [NM_005727]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1254	A_33_P3416142	2,321	up	LOC100131234	Homo sapiens familial acute myelogenous leukemia related factor mRNA, complete cds, [EF413001]
1255	A_23_P41599	2,321	up	PCDHB8	Homo sapiens protocadherin beta 8 (PCDHB8), mRNA [NM_019120]
1256	A_32_P216635	2,319	up	KSR2	Homo sapiens kinase suppressor of ras 2 (KSR2), mRNA [NM_173598]
1257	A_23_P348159	2,318	up	DST	dystonin [Source:HGNC Symbol;Acc:1090] [ENST00000439203]
1258	A_33_P3395428	2,317	up		Homo sapiens cDNA FLJ41314 fis, clone BRAMY2042918, [AK123308]
1259	A_23_P320225	2,317	up	EVC2	Homo sapiens Ellis van Creveld syndrome 2 (EVC2), transcript variant 1, mRNA [NM_147127]
1260	A_33_P3237879	2,315	up		Homo sapiens cDNA FLJ16652 fis, clone TESTI4036767, [AK131480]
1261	A_33_P3420816	2,315	up	GDF1	Homo sapiens growth differentiation factor 1 (GDF1), mRNA [NM_001492]
1262	A_33_P3412087	2,315	up	C6orf97	Homo sapiens chromosome 6 open reading frame 97 (C6orf97), mRNA [NM_025059]
1263	A_24_P254744	2,315	up	EPHA3	Homo sapiens EPH receptor A3 (EPHA3), transcript variant 2, mRNA [NM_182644]
1264	A_23_P334328	2,315	up	LAMB4	Homo sapiens laminin, beta 4 (LAMB4), mRNA [NM_007356]
1265	A_33_P3236426	2,314	up	FLJ16734	Homo sapiens cDNA FLJ16734 fis, clone BRACE2002589, [AK131514]
1266	A_32_P743184	2,314	up	DPPA3	Homo sapiens developmental pluripotency associated 3 (DPPA3), mRNA [NM_199286]
1267	A_33_P3510322	2,313	up		
1268	A_24_P83437	2,313	up	ZNF326	Homo sapiens zinc finger protein 326 (ZNF326), transcript variant 3, mRNA [NM_182975]
1269	A_23_P368154	2,312	up	PODN	Homo sapiens podocan (PODN), transcript variant 1, mRNA [NM_153703]
1270	A_33_P3238479	2,311	up	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila) [Source:HGNC Symbol;Acc:29150] [ENST00000381503]
1271	A_33_P3229472	2,310	up	KRTAP5-10	Homo sapiens keratin associated protein 5-10 (KRTAP5-10), mRNA [NM_001012710]
1272	A_23_P140614	2,310	up	LOC653061	Homo sapiens golgin A8 family, member B pseudogene (LOC653061), non-coding RNA [NR_038843]
1273	A_23_P7560	2,309	up	IL12B	Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), mRNA [NM_002187]
1274	A_24_P49427	2,308	up	KIAA1486	Homo sapiens KIAA1486 (KIAA1486), mRNA [NM_020864]
1275	A_33_P3272402	2,308	up	ADAD2	Homo sapiens adenosine deaminase domain containing 2 (ADAD2), transcript variant 1, mRNA [NM_139174]
1276	A_24_P333532	2,308	up	C8orf75	Homo sapiens chromosome 8 open reading frame 75 (C8orf75), non-coding RNA [NR_026765]
1277	A_24_P103893	2,307	up	HPSE2	Homo sapiens heparanase 2 (HPSE2), transcript variant 1, mRNA [NM_021828]
1278	A_33_P3379406	2,307	up	GREB1	Homo sapiens GREB1 protein, mRNA (cDNA clone IMAGE:6729261), partial cds, [BC071853]
1279	A_23_P409888	2,306	up	FAM83C	Homo sapiens family with sequence similarity 83, member C (FAM83C), mRNA [NM_178468]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1280	A_33_P3303245	2,305	up	KIT	Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), transcript variant 2, mRNA [NM_001093772]
1281	A_24_P400044	2,304	up	NUDT10	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 10 (NUDT10), mRNA [NM_153183]
1282	A_23_P95640	2,304	up	C1orf186	Homo sapiens chromosome 1 open reading frame 186 (C1orf186), mRNA [NM_001007544]
1283	A_23_P407112	2,303	up	SPATA18	Homo sapiens spermatogenesis associated 18 homolog (rat) (SPATA18), mRNA [NM_145263]
1284	A_23_P27133	2,303	up	KRT15	Homo sapiens keratin 15 (KRT15), mRNA [NM_002275]
1285	A_33_P3628675	2,302	up	FAM86B1	Homo sapiens family with sequence similarity 86, member B1 (FAM86B1), transcript variant 1, mRNA [NM_001083537]
1286	A_23_P164927	2,302	up	SYNGR4	Homo sapiens synaptogyrin 4 (SYNGR4), mRNA [NM_012451]
1287	A_33_P3236137	2,300	up	HYDIN	Homo sapiens hydrocephalus inducing homolog (mouse) (HYDIN), transcript variant 1, mRNA [NM_032821]
1288	A_33_P3259457	2,300	up		PREDICTED: Homo sapiens golgin-like (LOC441728), miscRNA [XR_109175]
1289	A_23_P365060	2,300	up	MDN1	Homo sapiens MDN1, midasin homolog (yeast) (MDN1), mRNA [NM_014611]
1290	A_33_P3303309	2,298	up	LOC150622	Homo sapiens hypothetical LOC150622 (LOC150622), non-coding RNA [NR_026832]
1291	A_23_P210164	2,298	up	HOXD8	Homo sapiens homeobox D8 (HOXD8), transcript variant 1, mRNA [NM_019558]
1292	A_24_P83899	2,298	up	GRM5	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), transcript variant b, mRNA [NM_000842]
1293	A_33_P3263392	2,297	up	LOC729696	Homo sapiens cDNA FLJ44161 fis, clone THYMU2033070, [AK126149]
1294	A_33_P3262292	2,297	up	UBXN7	Homo sapiens UBX domain protein 7 (UBXN7), mRNA [NM_015562]
1295	A_33_P3278635	2,297	up	TXNDC8	Homo sapiens thioredoxin domain containing 8 (spermatozoa) (TXNDC8), mRNA [NM_001003936]
1296	A_33_P3346680	2,296	up		GB
1297	A_33_P3338152	2,295	up	HIF3A	hypoxia inducible factor 3, alpha subunit [Source:HGNC Symbol;Acc:15825] [ENST00000457865]
1298	A_23_P147839	2,294	up	EPHA5	Homo sapiens EPH receptor A5 (EPHA5), transcript variant 1, mRNA [NM_004439]
1299	A_33_P3237492	2,294	up		ir69g09,y1 HR85 islet Homo sapiens cDNA clone IMAGE:6607866 5', mRNA sequence [CA849059]
1300	A_33_P3307049	2,294	up	LOC100129363	Homo sapiens cDNA FLJ46623 fis, clone TLUNG2001810, [AK128478]
1301	A_33_P3244117	2,294	up		Homo sapiens cDNA FLJ16106 fis, clone THYMU1000496, moderately similar to KINESIN-LIKE PROTEIN KIF1C, [AK122666]
1302	A_33_P3229241	2,294	up	HIST2H2BF	Homo sapiens histone cluster 2, H2bf (HIST2H2BF), transcript variant 1, mRNA [NM_001024599]
1303	A_24_P237778	2,293	up	MAN1C1	Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), mRNA [NM_020379]
1304	A_33_P3325384	2,292	up	LOC100130992	Homo sapiens hypothetical LOC100130992 (LOC100130992), non-coding RNA [NR_038921]
1305	A_33_P3386572	2,291	up	AGBL4	ATP/GTP binding protein-like 4 [Source:HGNC Symbol;Acc:25892] [ENST00000497451]
1306	A_33_P3223990	2,291	up	TPM3	Homo sapiens tropomyosin 3 (TPM3), transcript variant 1, mRNA [NM_152263]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1307	A_33_P3267185	2,291	up	ATP2B1	Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 1, mRNA [NM_001001323]
1308	A_33_P3361896	2,290	up	LOC100127994	Homo sapiens cDNA FLJ45631 fis, clone CHONS2001797, [AK127538]
1309	A_33_P3331351	2,290	up		
1310	A_33_P3317937	2,290	up	KRTAP20-1	Homo sapiens keratin associated protein 20-1 (KRTAP20-1), mRNA [NM_181615]
1311	A_33_P3221129	2,289	up	LRRN4CL	Homo sapiens LRRN4 C-terminal like (LRRN4CL), mRNA [NM_203422]
1312	A_33_P3246715	2,289	up	LOC441495	Homo sapiens centromere protein V pseudogene (LOC441495), non-coding RNA [NR_033773]
1313	A_33_P3333232	2,288	up		coiled-coil domain containing 162, pseudogene [Source:HGNC Symbol;Acc:21565] [ENST00000440451]
1314	A_23_P33984	2,287	up	TMEM27	Homo sapiens transmembrane protein 27 (TMEM27), mRNA [NM_020665]
1315	A_32_P202125	2,287	up	LOC100128988	full-length cDNA clone CS0DI068YN03 of Placenta Cot 25-normalized of Homo sapiens (human), [CR612573]
1316	A_33_P3210379	2,287	up	SCGB3A1	Homo sapiens secretoglobin, family 3A, member 1 (SCGB3A1), mRNA [NM_052863]
1317	A_33_P3224345	2,286	up		GB
1318	A_33_P3380582	2,285	up	LOC100508805	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase-like protein LOC641515 [Source:UniProtKB/Swiss-Prot;Acc:Q49AQ9] [ENST00000330493]
1319	A_33_P3214284	2,285	up		
1320	A_33_P3209806	2,285	up	OR2C3	Homo sapiens olfactory receptor, family 2, subfamily C, member 3 (OR2C3), mRNA [NM_198074]
1321	A_33_P3403963	2,285	up	ST8SIA6	Homo sapiens ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6 (ST8SIA6), mRNA [NM_001004470]
1322	A_33_P3316835	2,284	up	C4orf21	chromosome 4 open reading frame 21 [Source:HGNC Symbol;Acc:25654] [ENST00000264370]
1323	A_23_P103328	2,284	up	PTGER3	Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 4, mRNA [NM_198714]
1324	A_24_P634768	2,284	up	FLJ22763	Homo sapiens hypothetical LOC401081 (FLJ22763), non-coding RNA [NR_033977]
1325	A_33_P3509233	2,284	up	LOC285286	PREDICTED: Homo sapiens hypothetical LOC285286 (LOC285286), partial miscRNA [XR_109995]
1326	A_23_P58869	2,282	up	GSTM2P1	Homo sapiens glutathione S-transferase mu 2 (muscle) pseudogene 1 (GSTM2P1), non-coding RNA [NR_002932]
1327	A_23_P141142	2,282	up	QRICH2	Homo sapiens glutamine rich 2 (QRICH2), mRNA [NM_032134]
1328	A_33_P3378383	2,281	up	DNM1P46	Homo sapiens DNM1 pseudogene 46 (DNM1P46), non-coding RNA [NR_003260]
1329	A_33_P3591810	2,281	up		epidermal growth factor receptor pathway substrate 15 pseudogene 1 [Source:HGNC Symbol;Acc:18166] [ENST00000459691]
1330	A_33_P3291976	2,280	up	TERF1	telomeric repeat binding factor (NIMA-interacting) 1 [Source:HGNC Symbol;Acc:11728] [ENST00000518695]
1331	A_23_P163209	2,280	up	BCL2L10	Homo sapiens BCL2-like 10 (apoptosis facilitator) (BCL2L10), mRNA [NM_020396]
1332	A_33_P3252954	2,278	up	NKD2	naked cuticle homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:17046] [ENST00000382730]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1333	A_33_P3356106	2,278	up		
1334	A_33_P3406939	2,277	up	KIF24	Homo sapiens kinesin family member 24 (KIF24), mRNA [NM_194313]
1335	A_23_P58407	2,276	up	UGT2B15	Homo sapiens UDP glucuronosyltransferase 2 family, polypeptide B15 (UGT2B15), mRNA [NM_001076]
1336	A_33_P3407034	2,276	up	KIT	Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), transcript variant 1, mRNA [NM_000222]
1337	A_33_P3342190	2,276	up	LOC100133580	PREDICTED: Homo sapiens hypothetical protein LOC100133580 (LOC100133580), mRNA [XM_001715356]
1338	A_24_P693321	2,276	up	LOC100190986	Homo sapiens hypothetical LOC100190986 (LOC100190986), non-coding RNA [NR_024456]
1339	A_24_P330796	2,276	up	MKS1	Homo sapiens Meckel syndrome, type 1 (MKS1), transcript variant 1, mRNA [NM_017777]
1340	A_33_P3423210	2,275	up		
1341	A_33_P3213419	2,275	up	LOC100129447	Homo sapiens cDNA FLJ30384 fis, clone BRACE2008114, [AK054946]
1342	A_33_P3254073	2,275	up	C9orf68	chromosome 9 open reading frame 68 [Source:HGNC Symbol;Acc:25472] [ENST00000471669]
1343	A_33_P3367780	2,275	up	TMEM215	Homo sapiens transmembrane protein 215 (TMEM215), mRNA [NM_212558]
1344	A_33_P3277826	2,274	up	ZSCAN1	zinc finger and SCAN domain containing 1 [Source:HGNC Symbol;Acc:23712] [ENST00000391700]
1345	A_33_P3212221	2,274	up	DEPDC5	Homo sapiens DEP domain containing 5 (DEPDC5), transcript variant 2, mRNA [NM_001007188]
1346	A_32_P139738	2,274	up	HERC2P4	Homo sapiens hect domain and RLD 2 pseudogene 4 (HERC2P4), non-coding RNA [NR_002827]
1347	A_33_P3227676	2,273	up	C2orf72	Homo sapiens chromosome 2 open reading frame 72 (C2orf72), mRNA [NM_001144994]
1348	A_23_P46829	2,273	up	FGF8	Homo sapiens fibroblast growth factor 8 (androgen-induced) (FGF8), transcript variant F, mRNA [NM_033163]
1349	A_33_P3421338	2,273	up	KIF18B	Homo sapiens kinesin family member 18B (KIF18B), mRNA [NM_001080443]
1350	A_23_P313981	2,271	up	SERPINB10	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 10 (SERPINB10), mRNA [NM_005024]
1351	A_33_P3306207	2,271	up	KLRG2	Homo sapiens killer cell lectin-like receptor subfamily G, member 2 (KLRG2), mRNA [NM_198508]
1352	A_23_P119611	2,270	up	FXYD7	Homo sapiens FXYD domain containing ion transport regulator 7 (FXYD7), mRNA [NM_022006]
1353	A_23_P48663	2,270	up	OTX2	Homo sapiens orthodenticle homeobox 2 (OTX2), transcript variant 1, mRNA [NM_021728]
1354	A_33_P3295173	2,269	up	HSPB11	heat shock protein family B (small), member 11 [Source:HGNC Symbol;Acc:25019] [ENST00000371377]
1355	A_33_P3371360	2,269	up	C6orf186	Homo sapiens chromosome 6 open reading frame 186 (C6orf186), mRNA [NM_001123364]
1356	A_23_P404059	2,268	up	PASD1	Homo sapiens PAS domain containing 1 (PASD1), mRNA [NM_173493]
1357	A_32_P111639	2,268	up	CHST9	Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA [NM_031422]
1358	A_33_P3224675	2,268	up	CCDC76	coiled-coil domain containing 76 [Source:HGNC Symbol;Acc:25502] [ENST00000370139]
1359	A_33_P3241145	2,268	up		Homo sapiens cDNA clone IMAGE:5273698, [BC047414]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1360	A_33_P3239455	2,266	up	GTF2IRD2	Homo sapiens GTF2I repeat domain containing 2 (GTF2IRD2), mRNA [NM_173537]
1361	A_33_P3394995	2,266	up	PREX2	Homo sapiens phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2 (PREX2), transcript variant 2, mRNA [NM_025170]
1362	A_33_P3387601	2,266	up	KLKP1	Homo sapiens kallikrein pseudogene 1 (KLKP1), non-coding RNA [NR_002948]
1363	A_33_P3292588	2,266	up	UBTFL1	Homo sapiens upstream binding transcription factor, RNA polymerase I-like 1 (UBTFL1), mRNA [NM_001143975]
1364	A_33_P3406651	2,265	up	ZSCAN5B	Homo sapiens zinc finger and SCAN domain containing 5B (ZSCAN5B), mRNA [NM_001080456]
1365	A_23_P43690	2,264	up	BNC2	Homo sapiens basonuclin 2 (BNC2), mRNA [NM_017637]
1366	A_33_P3380797	2,263	up	FGF3	Homo sapiens fibroblast growth factor 3 (FGF3), mRNA [NM_005247]
1367	A_33_P3307836	2,262	up	LRRC7	leucine rich repeat containing 7 [Source:HGNC Symbol;Acc:18531] [ENST00000370958]
1368	A_33_P3209716	2,262	up	CTNND1	Homo sapiens catenin (cadherin-associated protein), delta 1 (CTNND1), transcript variant 16, mRNA [NM_001206885]
1369	A_33_P3331646	2,262	up		Homo sapiens cDNA clone IMAGE:5172092, [BC029877]
1370	A_24_P290225	2,261	up	HS3ST4	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA [NM_006040]
1371	A_33_P3221284	2,260	up	CCDC80	Homo sapiens coiled-coil domain containing 80 (CCDC80), transcript variant 1, mRNA [NM_199511]
1372	A_33_P3230676	2,260	up		
1373	A_23_P54968	2,260	up	ST6GALNAC1	Homo sapiens ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 (ST6GALNAC1), mRNA [NM_018414]
1374	A_33_P3282325	2,260	up	DAZ1	Homo sapiens deleted in azoospermia 1 (DAZ1), mRNA [NM_004081]
1375	A_33_P3229412	2,260	up	NRG3	Homo sapiens neuregulin 3 (NRG3), transcript variant 1, mRNA [NM_001010848]
1376	A_33_P3216610	2,259	up	TMPRSS4	Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 1, mRNA [NM_019894]
1377	A_23_P161458	2,258	up	OLAH	Homo sapiens oleoyl-ACP hydrolase (OLAH), transcript variant 2, mRNA [NM_001039702]
1378	A_33_P3408938	2,258	up	LILRP2	Homo sapiens leukocyte immunoglobulin-like receptor pseudogene 2 (LILRP2), non-coding RNA [NR_003061]
1379	A_23_P92196	2,258	up	RETNLB	Homo sapiens resistin like beta (RETNLB), mRNA [NM_032579]
1380	A_33_P3214803	2,258	up	PRDM13	Homo sapiens PR domain containing 13 (PRDM13), mRNA [NM_021620]
1381	A_23_P434289	2,256	up	GPR62	Homo sapiens G protein-coupled receptor 62 (GPR62), mRNA [NM_080865]
1382	A_33_P3307795	2,256	up	FAM124B	family with sequence similarity 124B [Source:HGNC Symbol;Acc:26224] [ENST00000243806]
1383	A_33_P3223663	2,256	up		
1384	A_33_P3354176	2,255	up	MYOF	myoferlin [Source:HGNC Symbol;Acc:3656] [ENST00000371488]
1385	A_33_P3419831	2,255	up		chromosome 20 open reading frame 62 [Source:HGNC Symbol;Acc:16195] [ENST00000306731]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1386	A_23_P170534	2,255	up	FUT7	Homo sapiens fucosyltransferase 7 (alpha (1,3) fucosyltransferase) (FUT7), mRNA [NM_004479]
1387	A_33_P3336514	2,254	up		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:A8MQ56] [ENST00000552123]
1388	A_33_P3278881	2,253	up	FLJ45340	Homo sapiens hypothetical LOC402483 (FLJ45340), non-coding RNA [NR_024368]
1389	A_23_P51761	2,252	up	OR6K2	Homo sapiens olfactory receptor, family 6, subfamily K, member 2 (OR6K2), mRNA [NM_001005279]
1390	A_33_P3281745	2,251	up		17000600021474 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence [CN291113]
1391	A_33_P3292148	2,249	up		PREDICTED: Homo sapiens hCG2044152 (LOC729224), partial miscRNA [XR_113421]
1392	A_23_P207213	2,249	up	ALDH3A1	Homo sapiens aldehyde dehydrogenase 3 family, member A1 (ALDH3A1), transcript variant 2, mRNA [NM_000691]
1393	A_33_P3358712	2,249	up	GRINL1A	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A (GRINL1A), transcript variant 3, non-coding RNA [NR_027390]
1394	A_33_P3238969	2,249	up	ONECUT3	Homo sapiens one cut homeobox 3 (ONECUT3), mRNA [NM_001080488]
1395	A_33_P3396224	2,249	up	C12orf69	Homo sapiens chromosome 12 open reading frame 69 (C12orf69), mRNA [NM_001013698]
1396	A_23_P40657	2,248	up	GCAT	Homo sapiens glycine C-acetyltransferase (GCAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_014291]
1397	A_23_P23783	2,248	up	MYOC	Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), mRNA [NM_000261]
1398	A_23_P258887	2,247	up	ALDH1L1	Homo sapiens aldehyde dehydrogenase 1 family, member L1 (ALDH1L1), mRNA [NM_012190]
1399	A_24_P55496	2,247	up	OSR2	Homo sapiens odd-skipped related 2 (Drosophila) (OSR2), transcript variant 2, mRNA [NM_053001]
1400	A_23_P208085	2,246	up	MBP	Homo sapiens myelin basic protein (MBP), transcript variant 7, mRNA [NM_001025101]
1401	A_33_P3388527	2,246	up		
1402	A_33_P3238820	2,246	up		
1403	A_33_P3278191	2,246	up		
1404	A_33_P3241741	2,245	up	SNORA23	Homo sapiens small nucleolar RNA, H/ACA box 23 (SNORA23), small nucleolar RNA [NR_002962]
1405	A_33_P3217427	2,245	up	DNAJC16	DnaJ (Hsp40) homolog, subfamily C, member 16 [Source:HGNC Symbol;Acc:29157] [ENST00000375838]
1406	A_33_P3257553	2,244	up	CNTRL	centrosomal protein 110kDa [Source:HGNC Symbol;Acc:1858] [ENST00000373847]
1407	A_33_P3285195	2,244	up	LOC100507012	PREDICTED: Homo sapiens hypothetical LOC100507012 (LOC100507012), partial miscRNA [XR_109821]
1408	A_23_P381017	2,242	up	WBSCR27	Homo sapiens Williams Beuren syndrome chromosome region 27 (WBSCR27), mRNA [NM_152559]
1409	A_23_P250694	2,241	up	TSGA13	Homo sapiens testis specific, 13 (TSGA13), mRNA [NM_052933]
1410	A_33_P3400152	2,240	up	LOC728558	Homo sapiens hypothetical LOC728558 (LOC728558), non-coding RNA [NR_038444]
1411	A_33_P3310562	2,240	up		Homo sapiens mRNA sequence, [AY927497]
1412	A_33_P3265783	2,240	up	STATH	Homo sapiens statherin (STATH), transcript variant 1, mRNA [NM_003154]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1413	A_33_P3329153	2,240	up	CDK13	Homo sapiens cyclin-dependent kinase 13 (CDK13), transcript variant 2, mRNA [NM_031267]
1414	A_24_P16913	2,239	up	ABCC4	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), transcript variant 1, mRNA [NM_005845]
1415	A_33_P3398513	2,239	up	LOC728819	Homo sapiens hCG1645220 (LOC728819), mRNA [NM_001101330]
1416	A_33_P3409277	2,237	up		1008982 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens cDNA 5', mRNA sequence [CB270075]
1417	A_23_P60599	2,237	up	UGT1A6	Homo sapiens UDP glucuronosyltransferase 1 family, polypeptide A6 (UGT1A6), transcript variant 1, mRNA [NM_001072]
1418	A_23_P92754	2,236	up	FGFR4	Homo sapiens fibroblast growth factor receptor 4 (FGFR4), transcript variant 3, mRNA [NM_213647]
1419	A_23_P367586	2,236	up	DNHD1	Homo sapiens dynein heavy chain domain 1 (DNHD1), transcript variant 2, mRNA [NM_173589]
1420	A_33_P3662685	2,236	up	DEFA9P	Homo sapiens defensin alpha 9 (DEFA9P) pseudogene mRNA, complete sequence, [AY746434]
1421	A_24_P375761	2,235	up	STGC3	PREDICTED: Homo sapiens hypothetical STGC3 (STGC3), miscRNA [XR_110003]
1422	A_33_P3346891	2,235	up	MYBL1	Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1), transcript variant 2, mRNA [NM_001144755]
1423	A_33_P3384272	2,235	up	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:799] [ENST00000369494]
1424	A_24_P153763	2,234	up		Homo sapiens cDNA clone IMAGE:3931942, partial cds, [BC015129]
1425	A_24_P68183	2,234	up	EGFEM1P	Homo sapiens EGF-like and EMI domain containing 1, pseudogene (EGFEM1P), non-coding RNA [NR_021485]
1426	A_33_P3270793	2,234	up	FAM84A	Homo sapiens family with sequence similarity 84, member A (FAM84A), mRNA [NM_145175]
1427	A_33_P3763412	2,231	up		Homo sapiens cDNA FLJ40109 fis, clone TESTI2007685, [AK097428]
1428	A_33_P3312384	2,231	up	C21orf34	Homo sapiens chromosome 21 open reading frame 34 (C21orf34), transcript variant 1, non-coding RNA [NR_027790]
1429	A_33_P3330384	2,231	up	BET1L	Homo sapiens blocked early in transport 1 homolog (S, cerevisiae)-like (BET1L), transcript variant 2, mRNA [NM_016526]
1430	A_33_P3221432	2,231	up	ZNF284	Homo sapiens zinc finger protein 284 (ZNF284), mRNA [NM_001037813]
1431	A_33_P3280875	2,230	up	IVNS1ABP	Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), mRNA [NM_006469]
1432	A_33_P3256844	2,229	up	WDR49	WD repeat domain 49 [Source:HGNC Symbol;Acc:26587] [ENST00000453925]
1433	A_33_P3236846	2,228	up	GPR17	Homo sapiens G protein-coupled receptor 17 (GPR17), transcript variant 1, mRNA [NM_001161415]
1434	A_33_P3469673	2,228	up	LOC284576	Homo sapiens hypothetical LOC284576 (LOC284576), non-coding RNA [NR_038425]
1435	A_23_P431853	2,228	up	ND2	mitochondrially encoded NADH dehydrogenase 2 [Source:HGNC Symbol;Acc:7456] [ENST00000361453]
1436	A_23_P42855	2,228	up	C7orf62	Homo sapiens chromosome 7 open reading frame 62 (C7orf62), mRNA [NM_152706]
1437	A_33_P3250944	2,228	up	C1orf189	Homo sapiens chromosome 1 open reading frame 189 (C1orf189), mRNA [NM_001010979]
1438	A_33_P3305617	2,227	up	C3orf57	chromosome 3 open reading frame 57 [Source:HGNC Symbol;Acc:24045] [ENST00000359175]
1439	A_33_P3365601	2,227	up		Q9WVL8_MOUSE (Q9WVL8) Zinc finger type transcription factor MZF-3, partial (25%) [THC2540172]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1440	A_33_P3228622	2,227	up	OR14I1	Homo sapiens olfactory receptor, family 14, subfamily I, member 1 (OR14I1), mRNA [NM_001004734]
1441	A_23_P85082	2,226	up	RHOXF1	Homo sapiens Rhox homeobox family, member 1 (RHOXF1), mRNA [NM_139282]
1442	A_33_P3220025	2,226	up	GOLGA6L6	Homo sapiens golgin A6 family-like 6 (GOLGA6L6), mRNA [NM_001145004]
1443	A_33_P3229288	2,226	up	ACE	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 (ACE), transcript variant 1, mRNA [NM_000789]
1444	A_33_P3229037	2,226	up		
1445	A_33_P3303176	2,226	up	MRGPRG	Homo sapiens MAS-related GPR, member G (MRGPRG), mRNA [NM_001164377]
1446	A_33_P3378680	2,225	up	ARHGAP26	Rho GTPase activating protein 26 [Source:HGNC Symbol;Acc:17073] [ENST00000378013]
1447	A_33_P3357678	2,224	up	LCTL	Homo sapiens lactase-like (LCTL), mRNA [NM_207338]
1448	A_23_P328034	2,224	up	C20orf96	Homo sapiens chromosome 20 open reading frame 96 (C20orf96), transcript variant 1, mRNA [NM_153269]
1449	A_23_P163492	2,224	up	BAIAP3	Homo sapiens BAI1-associated protein 3 (BAIAP3), transcript variant 1, mRNA [NM_003933]
1450	A_23_P397208	2,223	up	GSTM2	Homo sapiens glutathione S-transferase mu 2 (muscle) (GSTM2), transcript variant 1, mRNA [NM_000848]
1451	A_33_P3396431	2,223	up		HUMHAMRT reverse transcriptase {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (7%) [THC2620859]
1452	A_32_P58513	2,222	up	NCRNA00238	Homo sapiens non-protein coding RNA 238 (NCRNA00238), transcript variant 1, non-coding RNA [NR_024338]
1453	A_32_P88262	2,221	up	SLC7A14	Homo sapiens solute carrier family 7 (orphan transporter), member 14 (SLC7A14), mRNA [NM_020949]
1454	A_33_P3267410	2,221	up	KLLN	Homo sapiens killin, p53-regulated DNA replication inhibitor (KLLN), mRNA [NM_001126049]
1455	A_33_P3259028	2,221	up	TRIM24	tripartite motif containing 24 [Source:HGNC Symbol;Acc:11812] [ENST00000378381]
1456	A_33_P3329557	2,220	up		
1457	A_33_P3306828	2,220	up	ZNF806	PREDICTED: Homo sapiens zinc finger protein 806 (ZNF806), mRNA [XM_002345581]
1458	A_23_P73667	2,220	up	RIBC1	Homo sapiens RIB43A domain with coiled-coils 1 (RIBC1), transcript variant 1, mRNA [NM_001031745]
1459	A_33_P3307192	2,220	up		
1460	A_24_P233078	2,220	up	PYY2	Homo sapiens peptide YY, 2 (seminalplasmin) (PYY2), non-coding RNA [NR_003064]
1461	A_33_P3284247	2,219	up		glycogenin 2 pseudogene 1 [Source:HGNC Symbol;Acc:4701] [ENST00000382966]
1462	A_23_P207461	2,219	up	CA10	Homo sapiens carbonic anhydrase X (CA10), transcript variant 2, mRNA [NM_020178]
1463	A_24_P21770	2,219	up	YPEL4	Homo sapiens yippee-like 4 (Drosophila) (YPEL4), mRNA [NM_145008]
1464	A_33_P3589819	2,218	up	LOC100507637	Homo sapiens cDNA: FLJ22849 fis, clone KAIA987, [AK026502]
1465	A_33_P3232995	2,218	up	TDRD1	Homo sapiens tudor domain containing 1 (TDRD1), mRNA [NM_198795]
1466	A_33_P3354514	2,218	up	SLC2A13	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13, mRNA (cDNA clone MGC:48624 IMAGE:5272386), complete

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
					cds, [BC047507]
1467	A_23_P375922	2,217	up	COL19A1	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA [NM_001858]
1468	A_24_P316257	2,217	up	NHLRC4	Homo sapiens NHL repeat containing 4 (NHLRC4), mRNA [NM_176677]
1469	A_23_P2271	2,216	up	PTHLH	Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 1, mRNA [NM_198965]
1470	A_23_P146111	2,216	up	NIPAL2	Homo sapiens NIPA-like domain containing 2 (NIPAL2), mRNA [NM_024759]
1471	A_23_P338534	2,215	up	HIF3A	Homo sapiens hypoxia inducible factor 3, alpha subunit (HIF3A), transcript variant 2, mRNA [NM_022462]
1472	A_33_P3712341	2,214	up	CXCL12	Homo sapiens chemokine (C-X-C motif) ligand 12 (CXCL12), transcript variant 3, mRNA [NM_001033886]
1473	A_33_P3331335	2,214	up	TET3	Homo sapiens tet oncogene family member 3 (TET3), mRNA [NM_144993]
1474	A_33_P3262421	2,214	up		Homo sapiens mRNA for KIAA1659 protein, partial cds, [AB051446]
1475	A_23_P111724	2,213	up	RUNDC3B	Homo sapiens RUN domain containing 3B (RUNDC3B), transcript variant 1, mRNA [NM_138290]
1476	A_33_P3400319	2,213	up		PREDICTED: Homo sapiens hypothetical LOC151760 (LOC151760), miscRNA [XR_108461]
1477	A_24_P667968	2,212	up	DKFZP434A062	Homo sapiens hypothetical LOC26102 (DKFZP434A062), non-coding RNA [NR_026964]
1478	A_33_P3316078	2,211	up	INTS6	Homo sapiens integrator complex subunit 6 (INTS6), transcript variant 3, mRNA [NM_001039938]
1479	A_33_P3373715	2,210	up		coatomer protein complex, subunit gamma 2 [Source:HGNC Symbol;Acc:2237] [ENST00000445977]
1480	A_23_P72912	2,210	up	SLC4A8	Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8), transcript variant 2, mRNA [NM_004858]
1481	A_33_P3276217	2,209	up		
1482	A_23_P328145	2,209	up	FAM71D	Homo sapiens family with sequence similarity 71, member D (FAM71D), mRNA [NM_173526]
1483	A_33_P3330826	2,209	up	LOC100132077	Homo sapiens hypothetical LOC100132077 (LOC100132077), non-coding RNA [NR_033937]
1484	A_23_P45976	2,208	up	RAP1GAP	Homo sapiens RAP1 GTPase activating protein (RAP1GAP), transcript variant 3, mRNA [NM_002885]
1485	A_33_P3345952	2,207	up	LOC100129213	Homo sapiens hypothetical LOC100129213 (LOC100129213), non-coding RNA [NR_038419]
1486	A_33_P3343101	2,204	up	ARGLU1	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:25482] [ENST00000426600]
1487	A_23_P217570	2,204	up	CAPN6	Homo sapiens calpain 6 (CAPN6), mRNA [NM_014289]
1488	A_33_P3210620	2,204	up	LOC100131497	human full-length cDNA 5-PRIME end of clone CS0CAP002YE20 of Thymus of Homo sapiens (human), [BX248745]
1489	A_33_P3649472	2,203	up	LOC283856	Homo sapiens hypothetical LOC283856 (LOC283856), non-coding RNA [NR_027078]
1490	A_23_P93973	2,203	up	TRPV5	Homo sapiens transient receptor potential cation channel, subfamily V, member 5 (TRPV5), mRNA [NM_019841]
1491	A_24_P232790	2,203	up	C14orf162	Homo sapiens chromosome 14 open reading frame 162 (C14orf162), non-coding RNA [NR_024630]
1492	A_32_P440667	2,203	up	SYNPO2	Homo sapiens synaptopodin 2 (SYNPO2), transcript variant 2, mRNA [NM_001128933]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1493	A_32_P494620	2,202	up	LHFPL5	Homo sapiens lipoma HMGIC fusion partner-like 5 (LHFPL5), mRNA [NM_182548]
1494	A_33_P3270197	2,202	up	DIS3L2	Homo sapiens DIS3 mitotic control homolog (S, cerevisiae)-like 2 (DIS3L2), mRNA [NM_152383]
1495	A_23_P136116	2,201	up	AGMO	Homo sapiens alkylglycerol monooxygenase (AGMO), mRNA [NM_001004320]
1496	A_32_P23308	2,201	up	LOC257358	Homo sapiens hypothetical LOC257358 (LOC257358), non-coding RNA [NR_026945]
1497	A_23_P105251	2,201	up	GLI1	Homo sapiens GLI family zinc finger 1 (GLI1), transcript variant 1, mRNA [NM_005269]
1498	A_33_P3243028	2,200	up	DSPP	Homo sapiens dentin sialophosphoprotein (DSPP), mRNA [NM_014208]
1499	A_23_P134729	2,200	up	C8orf39	Homo sapiens chromosome 8 open reading frame 39 (C8orf39), non-coding RNA [NR_027259]
1500	A_24_P100190	2,200	up	NCRNA00315	PREDICTED: Homo sapiens chromosome 21 open reading frame 93 (C21orf93), miscRNA [XR_109683]
1501	A_23_P312837	2,199	up	C9orf70	Homo sapiens chromosome 9 open reading frame 70 (C9orf70), non-coding RNA [NR_026663]
1502	A_33_P3423984	2,199	up	PALLD	palladin, cytoskeletal associated protein [Source:HGNC Symbol;Acc:17068] [ENST00000333488]
1503	A_23_P132760	2,199	up	TRH	Homo sapiens thyrotropin-releasing hormone (TRH), mRNA [NM_007117]
1504	A_33_P3419108	2,198	up	PRY2	Homo sapiens PTPN13-like, Y-linked 2 (PRY2), mRNA [NM_001002758]
1505	A_33_P3323979	2,198	up	LOC339874	Homo sapiens hypothetical LOC339874 (LOC339874), non-coding RNA [NR_038976]
1506	A_33_P3376546	2,198	up	PTGFR	Homo sapiens prostaglandin F receptor (FP) (PTGFR), transcript variant 2, mRNA [NM_001039585]
1507	A_33_P3421703	2,198	up	SP2	Sp2 transcription factor [Source:HGNC Symbol;Acc:11207] [ENST00000322172]
1508	A_33_P3397940	2,197	up		Homo sapiens cDNA FLJ46692 fis, clone TRACH3012718, [AK128534]
1509	A_33_P3311992	2,197	up	MAGI2	Homo sapiens membrane associated guanylate kinase, WW and PDZ domain containing 2 (MAGI2), mRNA [NM_012301]
1510	A_33_P3342569	2,197	up		Putative UPF0607 protein FLJ37424 [Source:UniProtKB/Swiss-Prot;Acc:Q8N9G6] [ENST00000359888]
1511	A_33_P3256972	2,196	up	ACTL7B	Homo sapiens actin-like 7B (ACTL7B), mRNA [NM_006686]
1512	A_33_P3381097	2,196	up	OR10V1	Homo sapiens olfactory receptor, family 10, subfamily V, member 1 (OR10V1), mRNA [NM_001005324]
1513	A_23_P169873	2,196	up	TRPC2	Homo sapiens transient receptor potential cation channel, subfamily C, member 2, pseudogene (TRPC2), non-coding RNA [NR_002720]
1514	A_33_P3312504	2,196	up	PSD4	Homo sapiens pleckstrin and Sec7 domain containing 4 (PSD4), mRNA [NM_012455]
1515	A_23_P107483	2,196	up	OR3A3	Homo sapiens olfactory receptor, family 3, subfamily A, member 3 (OR3A3), mRNA [NM_012373]
1516	A_33_P3221888	2,196	up		
1517	A_33_P3327300	2,195	up	LOC100130713	Homo sapiens cDNA FLJ39247 fis, clone OCBBF2008520, [AK096566]
1518	A_33_P3259293	2,195	up	SLC37A3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3 [Source:HGNC Symbol;Acc:20651] [ENST00000493423]
1519	A_33_P3401169	2,194	up		T cell receptor beta variable 21/OR9-2 (non-functional) [Source:HGNC Symbol;Acc:12199] [ENST00000331828]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1520	A_33_P3318763	2,194	up		
1521	A_24_P247732	2,194	up	SLC5A6	Homo sapiens solute carrier family 5 (sodium-dependent vitamin transporter), member 6 (SLC5A6), transcript variant 1, mRNA [NM_021095]
1522	A_33_P3352253	2,193	up	MTUS1	Homo sapiens microtubule associated tumor suppressor 1 (MTUS1), transcript variant 2, mRNA [NM_001001925]
1523	A_33_P3289162	2,193	up		stonin 1 [Source:HGNC Symbol;Acc:17003] [ENST00000484110]
1524	A_33_P3255354	2,192	up	NT5C2	Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), transcript variant 1, mRNA [NM_012229]
1525	A_23_P72697	2,192	up	GPIHBP1	Homo sapiens glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1 (GPIHBP1), mRNA [NM_178172]
1526	A_33_P3386562	2,191	up	AGBL4	Homo sapiens ATP/GTP binding protein-like 4 (AGBL4), mRNA [NM_032785]
1527	A_33_P3268974	2,191	up	RECQL5	Homo sapiens RecQ protein-like 5 (RECQL5), transcript variant 2, mRNA [NM_001003715]
1528	A_32_P8546	2,191	up	C6orf176	Homo sapiens chromosome 6 open reading frame 176 (C6orf176), transcript variant 1, non-coding RNA [NR_026860]
1529	A_23_P86532	2,191	up	BICC1	bicaudal C homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:19351] [ENST00000263103]
1530	A_33_P3334625	2,190	up	FLJ41327	Homo sapiens cDNA FLJ41327 fis, clone BRAMY2047169, [AK123321]
1531	A_33_P3225610	2,190	up		PREDICTED: Homo sapiens hypothetical protein LOC100507519 (LOC100507519), mRNA [XM_003118685]
1532	A_33_P3253877	2,189	up	TACC1	transforming, acidic coiled-coil containing protein 1 [Source:HGNC Symbol;Acc:11522] [ENST00000518415]
1533	A_33_P3362208	2,189	up	LOC100129233	PREDICTED: Homo sapiens hypothetical LOC100129233 (LOC100129233), miscRNA [XR_110553]
1534	A_33_P3284472	2,189	up	DDX51	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (DDX51), mRNA [NM_175066]
1535	A_33_P3337901	2,188	up	PDE4DIP	Homo sapiens phosphodiesterase 4D interacting protein (PDE4DIP), transcript variant 9, mRNA [NM_001198834]
1536	A_33_P3246193	2,188	up		chromosome 10 open reading frame 93 [Source:HGNC Symbol;Acc:26382] [ENST00000368582]
1537	A_24_P942346	2,187	up	ECT2L	Homo sapiens epithelial cell transforming sequence 2 oncogene-like (ECT2L), transcript variant 1, mRNA [NM_001077706]
1538	A_33_P3343720	2,187	up	CELA3A	Homo sapiens chymotrypsin-like elastase family, member 3A (CELA3A), mRNA [NM_005747]
1539	A_33_P3315659	2,186	up		
1540	A_33_P3402788	2,186	up		Homo sapiens, clone IMAGE:5393038, mRNA, [BC042181]
1541	A_23_P81103	2,186	up	SFRP2	Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA [NM_003013]
1542	A_24_P144773	2,186	up	RNF145	Homo sapiens ring finger protein 145 (RNF145), transcript variant 2, mRNA [NM_144726]
1543	A_33_P3358815	2,186	up	DEFB103A	Homo sapiens defensin, beta 103A (DEFB103A), mRNA [NM_001081551]
1544	A_33_P3415744	2,185	up	ANKRD36B	Homo sapiens ankyrin repeat domain 36B (ANKRD36B), mRNA [NM_025190]
1545	A_24_P331373	2,184	up	C22orf13	Homo sapiens chromosome 22 open reading frame 13 (C22orf13), mRNA [NM_031444]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1546	A_24_P162226	2,184	up	RIMBP2	Homo sapiens RIMS binding protein 2 (RIMBP2), mRNA [NM_015347]
1547	A_33_P3234048	2,184	up	LOC100131878	Homo sapiens cDNA FLJ43693 fis, clone TBAES2005543, [AK125681]
1548	A_23_P215070	2,184	up	TSGA14	Homo sapiens testis specific, 14 (TSGA14), mRNA [NM_018718]
1549	A_33_P3297883	2,184	up	LOC100131796	Homo sapiens LP2570 mRNA, complete cds, [AY203937]
1550	A_33_P3370244	2,183	up	LOC342346	Homo sapiens hypothetical protein LOC342346 (LOC342346), mRNA [NM_001145011]
1551	A_23_P135248	2,183	up	CCL27	Homo sapiens chemokine (C-C motif) ligand 27 (CCL27), mRNA [NM_006664]
1552	A_33_P3349252	2,183	up	DKFZP547L112	Homo sapiens mRNA; cDNA DKFZp547L112 (from clone DKFZp547L112), [AL512723]
1553	A_23_P34209	2,183	up	TTTY5	Homo sapiens testis-specific transcript, Y-linked 5 (non-protein coding) (TTTY5), non-coding RNA [NR_001541]
1554	A_33_P3361925	2,182	up	PHF8	Homo sapiens PHD finger protein 8 (PHF8), transcript variant 4, mRNA [NM_001184898]
1555	A_33_P3396776	2,182	up	C7orf66	Homo sapiens chromosome 7 open reading frame 66 (C7orf66), mRNA [NM_001024607]
1556	A_33_P3262449	2,182	up		golgin A6 family-like 2 [Source:HGNC Symbol;Acc:26695] [ENST00000312015]
1557	A_33_P3248982	2,181	up	FAIM2	Homo sapiens Fas apoptotic inhibitory molecule 2 (FAIM2), mRNA [NM_012306]
1558	A_33_P3282634	2,181	up	ALDH1L2	Homo sapiens aldehyde dehydrogenase 1 family, member L2 (ALDH1L2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_001034173]
1559	A_32_P410272	2,180	up		Homo sapiens cDNA clone IMAGE:6971743, partial cds, [BC066878]
1560	A_33_P3415350	2,179	up	KCNB2	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), mRNA [NM_004770]
1561	A_33_P3324454	2,179	up	TPP1	Homo sapiens tripeptidyl peptidase I (TPP1), mRNA [NM_000391]
1562	A_33_P3223701	2,178	up	SPATA16	Homo sapiens spermatogenesis associated 16 (SPATA16), mRNA [NM_031955]
1563	A_23_P65307	2,178	up	SLITRK6	Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA [NM_032229]
1564	A_33_P3262814	2,177	up	REEP3	Homo sapiens receptor accessory protein 3 (REEP3), mRNA [NM_001001330]
1565	A_33_P3341299	2,177	up	CACNG4	Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), mRNA [NM_014405]
1566	A_33_P3413483	2,177	up	SORD	Homo sapiens cDNA FLJ33419 fis, clone BRACE2019877, [AK090738]
1567	A_33_P3232339	2,176	up	LOC100129119	PREDICTED: Homo sapiens hypothetical LOC100129119, transcript variant 1 (LOC100129119), partial miscRNA [XR_109159]
1568	A_32_P161033	2,176	up		Homo sapiens, clone IMAGE:6155889, mRNA, [BC043411]
1569	A_33_P3285639	2,174	up	TSGA10	Homo sapiens testis specific, 10 (TSGA10), transcript variant 1, mRNA [NM_025244]
1570	A_33_P3373437	2,173	up		PREDICTED: Homo sapiens hypothetical LOC100129463 (LOC100129463), partial miscRNA [XR_108760]
1571	A_24_P306304	2,173	up	PRAMEF16	Homo sapiens PRAME family member 16 (PRAMEF16), mRNA [NM_001045480]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1572	A_33_P3298935	2,172	up	LOC646377	PREDICTED: Homo sapiens similar to hCG2041495 (LOC646377), mRNA [XM_001722743]
1573	A_23_P79217	2,172	up	LCT	Homo sapiens lactase (LCT), mRNA [NM_002299]
1574	A_33_P3378545	2,171	up		DB092099 TESTI4 Homo sapiens cDNA clone TESTI4041634 5', mRNA sequence [DB092099]
1575	A_33_P3337480	2,171	up	ZNF705A	Homo sapiens zinc finger protein 705A (ZNF705A), mRNA [NM_001004328]
1576	A_23_P25720	2,171	up	SERPINA4	Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4 (SERPINA4), mRNA [NM_006215]
1577	A_33_P3497502	2,171	up	LOC283475	Homo sapiens mRNA; cDNA DKFZp686K1548 (from clone DKFZp686K1548) [AL833568]
1578	A_33_P3356557	2,171	up	OR5D18	Homo sapiens olfactory receptor, family 5, subfamily D, member 18 (OR5D18), mRNA [NM_001001952]
1579	A_33_P3519424	2,170	up	LOC386597	Homo sapiens cDNA FLJ32573 fis, clone SPLEN2000210, [AK057135]
1580	A_23_P303851	2,170	up	TAS2R45	Homo sapiens taste receptor, type 2, member 45 (TAS2R45), mRNA [NM_176886]
1581	A_23_P130974	2,170	up	KIAA1683	Homo sapiens KIAA1683 (KIAA1683), transcript variant 2, mRNA [NM_025249]
1582	A_24_P295330	2,169	up	TSTD2	Homo sapiens thiosulfate sulfurtransferase (rhodanese)-like domain containing 2 (TSTD2), mRNA [NM_139246]
1583	A_32_P183442	2,169	up		601885412F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103859 5', mRNA sequence [BF217859]
1584	A_33_P3380196	2,169	up	AKAP9	Homo sapiens A kinase (PRKA) anchor protein (yotiao) 9, mRNA (cDNA clone IMAGE:3914749), complete cds, [BC015533]
1585	A_33_P3397525	2,167	up	WNT4	Homo sapiens wingless-type MMTV integration site family, member 4 (WNT4), mRNA [NM_030761]
1586	A_24_P81514	2,167	up	RPP30	Homo sapiens ribonuclease P/MRP 30kDa subunit (RPP30), transcript variant 2, mRNA [NM_006413]
1587	A_33_P3277659	2,166	up	ANKRD30B	Homo sapiens ankyrin repeat domain 30B (ANKRD30B), mRNA [NM_001145029]
1588	A_33_P3340094	2,166	up		PREDICTED: Homo sapiens FLJ45832 protein (FLJ45832), miscRNA [XR_110166]
1589	A_23_P111583	2,166	up	CD36	Homo sapiens CD36 molecule (thrombospondin receptor) (CD36), transcript variant 2, mRNA [NM_001001547]
1590	A_33_P3252800	2,165	up	PTPRR	Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA [NM_002849]
1591	A_23_P394259	2,165	up	MPP2	Homo sapiens membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2), mRNA [NM_005374]
1592	A_23_P502957	2,165	up	CDH26	Homo sapiens cadherin 26 (CDH26), transcript variant b, mRNA [NM_021810]
1593	A_33_P3247237	2,163	up	CIZ1	Homo sapiens CDKN1A interacting zinc finger protein 1 (CIZ1), transcript variant 2, mRNA [NM_001131015]
1594	A_33_P3287383	2,163	up	SLC22A2	solute carrier family 22 (organic cation transporter), member 2 [Source:HGNC Symbol;Acc:10966] [ENST00000366952]
1595	A_33_P3402116	2,163	up	EIF2C1	Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA [NM_012199]
1596	A_24_P340696	2,163	up	SERHL2	Homo sapiens serine hydrolase-like 2 (SERHL2), mRNA [NM_014509]
1597	A_32_P119569	2,162	up	GOLGA8E	Homo sapiens golgin A8 family, member E (GOLGA8E), non-coding RNA [NR_033350]
1598	A_33_P3227798	2,162	up	LOC100129995	Homo sapiens cDNA FLJ42448 fis, clone BRACE2003639, [AK124439]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1599	A_33_P3316661	2,162	up	C12orf42	chromosome 12 open reading frame 42 [Source:HGNC Symbol;Acc:24729] [ENST00000315192]
1600	A_33_P3383079	2,160	up		
1601	A_32_P212897	2,159	up	LOC643406	Homo sapiens hypothetical LOC643406 (LOC643406), non-coding RNA [NR_029405]
1602	A_24_P246636	2,158	up		
1603	A_33_P3243683	2,157	up	DIAPH1	Homo sapiens diaphanous homolog 1 (Drosophila) (DIAPH1), transcript variant 1, mRNA [NM_005219]
1604	A_23_P145930	2,157	up		
1605	A_33_P3387062	2,157	up		
1606	A_33_P3213518	2,157	up		
1607	A_33_P3289996	2,157	up	USP45	Homo sapiens ubiquitin specific peptidase 45 (USP45), mRNA [NM_001080481]
1608	A_23_P90743	2,156	up	REG1A	Homo sapiens regenerating islet-derived 1 alpha (REG1A), mRNA [NM_002909]
1609	A_33_P3564487	2,156	up	LOC285878	Homo sapiens hypothetical LOC285878 (LOC285878), non-coding RNA [NR_038994]
1610	A_23_P424126	2,156	up	ZNF354C	Homo sapiens zinc finger protein 354C (ZNF354C), mRNA [NM_014594]
1611	A_33_P3266998	2,155	up	FAM106CP	Homo sapiens family with sequence similarity 106, member C, pseudogene (FAM106CP), non-coding RNA [NR_026810]
1612	A_24_P158285	2,155	up	CYLC2	Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA [NM_001340]
1613	A_23_P381351	2,155	up	CSH1	Homo sapiens chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1), mRNA [NM_001317]
1614	A_24_P63380	2,155	up	BMPR1B	Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), mRNA [NM_001203]
1615	A_23_P207850	2,154	up	TNS4	Homo sapiens tensin 4 (TNS4), mRNA [NM_032865]
1616	A_33_P3389917	2,153	up	MTR	Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), mRNA [NM_000254]
1617	A_23_P64854	2,153	up	KRT75	Homo sapiens keratin 75 (KRT75), mRNA [NM_004693]
1618	A_33_P3317942	2,153	up		
1619	A_33_P3383724	2,152	up	TRIM61	Homo sapiens tripartite motif containing 61 (TRIM61), mRNA [NM_001012414]
1620	A_33_P3363082	2,152	up	SCARNA5	Homo sapiens small Cajal body-specific RNA 5 (SCARNA5), guide RNA [NR_003008]
1621	A_23_P27128	2,151	up	KLHL10	Homo sapiens kelch-like 10 (Drosophila) (KLHL10), mRNA [NM_152467]
1622	A_23_P121945	2,151	up	SNCB	Homo sapiens synuclein, beta (SNCB), transcript variant 1, mRNA [NM_001001502]
1623	A_23_P93641	2,151	up	AKR1B10	Homo sapiens aldo-keto reductase family 1, member B10 (aldose reductase) (AKR1B10), mRNA [NM_020299]
1624	A_23_P69326	2,151	up	CADPS	Homo sapiens Ca++-dependent secretion activator (CADPS), transcript variant 3, mRNA [NM_183393]
1625	A_33_P3349661	2,150	up	PCDH9	Homo sapiens protocadherin 9 (PCDH9), transcript variant 1, mRNA [NM_203487]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1626	A_33_P3311493	2,149	up	LOC283392	Homo sapiens hypothetical LOC283392 (LOC283392), transcript variant 2, non-coding RNA [NR_026836]
1627	A_33_P3375708	2,149	up		CG024_HUMAN (O75223) Protein C7orf24, partial (73%) [THC2569912]
1628	A_33_P3319331	2,149	up	PRDM2	Homo sapiens cDNA FLJ41611 fis, clone CTONG3002020, [AK123605]
1629	A_33_P3285602	2,148	up		MYCL2_HUMAN (P12525) L-myc-2 protein, complete [THC2602658]
1630	A_33_P3358432	2,148	up	LOC100507073	PREDICTED: Homo sapiens hypothetical LOC100507073 (LOC100507073), partial miscRNA [XR_109943]
1631	A_33_P3392405	2,148	up	C10orf99	Homo sapiens chromosome 10 open reading frame 99 (C10orf99), mRNA [NM_207373]
1632	A_33_P3287403	2,147	up		DA807153 OCBBF3 Homo sapiens cDNA clone OCBBF3022701 5', mRNA sequence [DA807153]
1633	A_33_P3398000	2,147	up	LOC100506866	Homo sapiens hypothetical LOC100506866 (LOC100506866), transcript variant 1, non-coding RNA [NR_038272]
1634	A_33_P3299349	2,147	up		
1635	A_23_P355517	2,147	up	SYNPO2L	Homo sapiens synaptopodin 2-like (SYNPO2L), transcript variant 2, mRNA [NM_024875]
1636	A_33_P3229380	2,147	up	LOC731275	Homo sapiens hypothetical LOC731275 (LOC731275), non-coding RNA [NR_029401]
1637	A_33_P3288384	2,147	up	PSMA1	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 1 (PSMA1), transcript variant 3, mRNA [NM_001143937]
1638	A_24_P177553	2,147	up		AGENCOURT_10615922 NIH_MGC_141 Homo sapiens cDNA clone IMAGE:6744194 5', mRNA sequence [BU963192]
1639	A_33_P3366540	2,147	up	CSGALNACT1	Homo sapiens chondroitin sulfate N-acetylgalactosaminyltransferase 1 (CSGALNACT1), transcript variant 1, mRNA [NM_001130518]
1640	A_33_P3301129	2,146	up		
1641	A_33_P3343045	2,146	up	CALHM2	calcium homeostasis modulator 2 [Source:HGNC Symbol;Acc:23493] [ENST00000393235]
1642	A_33_P3349774	2,146	up	LSM14B	Homo sapiens LSM14B, SCD6 homolog B (S, cerevisiae) (LSM14B), mRNA [NM_144703]
1643	A_33_P3219010	2,146	up	PPA2	pyrophosphatase (inorganic) 2 [Source:HGNC Symbol;Acc:28883] [ENST00000505713]
1644	A_32_P200308	2,145	up	LOC728724	Homo sapiens hCG1814486 (LOC728724), non-coding RNA [NR_033916]
1645	A_24_P577694	2,144	up	ADCY1	Homo sapiens adenylate cyclase 1 (brain) (ADCY1), mRNA [NM_021116]
1646	A_24_P40721	2,144	up	SPTLC3	Homo sapiens serine palmitoyltransferase, long chain base subunit 3 (SPTLC3), mRNA [NM_018327]
1647	A_33_P3377391	2,144	up		Q4NIX6_9MICC (Q4NIX6) Protein kinase, partial (4%) [THC2772049]
1648	A_32_P480177	2,143	up	TNN	Homo sapiens tenascin N (TNN), mRNA [NM_022093]
1649	A_24_P268729	2,143	up	HEMK1	Homo sapiens HemK methyltransferase family member 1 (HEMK1), mRNA [NM_016173]
1650	A_33_P3249958	2,143	up	LOC642852	Homo sapiens hypothetical LOC642852 (LOC642852), non-coding RNA [NR_026943]
1651	A_33_P3396591	2,143	up	FAM113A	Homo sapiens family with sequence similarity 113, member A (FAM113A), mRNA [NM_022760]
1652	A_33_P3213992	2,142	up		

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1653	A_23_P393099	2,142	up	TFF3	Homo sapiens trefoil factor 3 (intestinal) (TFF3), mRNA [NM_003226]
1654	A_33_P3415653	2,142	up	LOC100128668	Homo sapiens cDNA FLJ46166 fis, clone TESTI4002889, [AK128046]
1655	A_33_P3397298	2,140	up		
1656	A_33_P3411080	2,139	up	FSCN2	Homo sapiens fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus) (FSCN2), transcript variant 1, mRNA [NM_012418]
1657	A_23_P24211	2,139	up	MMP21	Homo sapiens matrix metallopeptidase 21 (MMP21), mRNA [NM_147191]
1658	A_24_P204043	2,139	up	ZNF318	Homo sapiens zinc finger protein 318 (ZNF318), mRNA [NM_014345]
1659	A_23_P35977	2,139	up	PDZD3	Homo sapiens PDZ domain containing 3 (PDZD3), transcript variant 2, mRNA [NM_024791]
1660	A_33_P3732844	2,139	up		Homo sapiens cDNA FLJ37566 fis, clone BRCOC2002085, [AK094885]
1661	A_33_P3227793	2,137	up	CGREF1	Homo sapiens cell growth regulator with EF-hand domain 1 (CGREF1), transcript variant 1, mRNA [NM_006569]
1662	A_33_P3325102	2,137	up	LOC644173	full-length cDNA clone CS0DC007YI01 of Neuroblastoma Cot 25-normalized of Homo sapiens (human), [CR604878]
1663	A_33_P3234859	2,137	up	UTRN	Homo sapiens utrophin (UTRN), mRNA [NM_007124]
1664	A_33_P3354214	2,137	up		
1665	A_33_P3220376	2,136	up		NP1L1_HUMAN (P55209) Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP), partial (38%) [THC2591311]
1666	A_24_P158468	2,136	up	C10orf91	Homo sapiens chromosome 10 open reading frame 91 (C10orf91), mRNA [NM_173541]
1667	A_23_P61042	2,136	up		immunoglobulin heavy constant alpha 2 (A2m marker) [Source:HGNC Symbol;Acc:5479] [ENST00000390539]
1668	A_33_P3407540	2,136	up	TRAPPC2	trafficking protein particle complex 2 [Source:HGNC Symbol;Acc:23068] [ENST00000380578]
1669	A_33_P3268612	2,136	up	IL28RA	Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 1, mRNA [NM_170743]
1670	A_33_P3253723	2,136	up	AQP1	Homo sapiens aquaporin 1 (Colton blood group) (AQP1), transcript variant 1, mRNA [NM_198098]
1671	A_33_P3287078	2,135	up	GZF1	Homo sapiens GDNF-inducible zinc finger protein 1 (GZF1), mRNA [NM_022482]
1672	A_33_P3308147	2,134	up		
1673	A_33_P3289810	2,134	up		PREDICTED: Homo sapiens extracellular matrix protein 2-like (LOC100507352), mRNA [XM_003119196]
1674	A_23_P55544	2,133	up	CCBE1	Homo sapiens collagen and calcium binding EGF domains 1 (CCBE1), mRNA [NM_133459]
1675	A_24_P246841	2,133	up	SLC25A27	Homo sapiens solute carrier family 25, member 27 (SLC25A27), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_004277]
1676	A_33_P3773374	2,133	up	LOC286063	Homo sapiens cDNA FLJ33573 fis, clone BRAMY2010798, [AK090892]
1677	A_33_P3308740	2,133	up	RANBP2	Homo sapiens RAN binding protein 2 (RANBP2), mRNA [NM_006267]
1678	A_33_P3217764	2,133	up		PREDICTED: Homo sapiens FLJ35816 protein (FLJ35816), miscRNA [XR_110582]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1679	A_33_P3356371	2,133	up	LOC100133089	Homo sapiens cDNA FLJ45867 fis, clone OCBBF3003745, [AK127766]
1680	A_24_P298027	2,132	up	AXIN2	Homo sapiens axin 2 (AXIN2), mRNA [NM_004655]
1681	A_33_P3318343	2,131	up	CTAG2	Homo sapiens cancer/testis antigen 2 (CTAG2), transcript variant 2, mRNA [NM_020994]
1682	A_24_P127748	2,131	up	CLASP2	Homo sapiens cytoplasmic linker associated protein 2 (CLASP2), transcript variant 1, mRNA [NM_015097]
1683	A_33_P3267033	2,130	up	LOC100130169	PREDICTED: Homo sapiens hypothetical LOC100130169 (LOC100130169), miscRNA [XR_108782]
1684	A_33_P3401661	2,129	up		
1685	A_23_P83634	2,129	up	ALOX12B	Homo sapiens arachidonate 12-lipoxygenase, 12R type (ALOX12B), mRNA [NM_001139]
1686	A_33_P3273173	2,129	up	USP11	Homo sapiens ubiquitin specific peptidase 11 (USP11), mRNA [NM_004651]
1687	A_33_P3462975	2,129	up	LOC401497	Homo sapiens cDNA clone IMAGE:4826624, [BC022036]
1688	A_32_P180210	2,128	up	FAM35A	Homo sapiens family with sequence similarity 35, member A (FAM35A), mRNA [NM_019054]
1689	A_33_P3576853	2,128	up	LOC254128	Homo sapiens hypothetical LOC254128 (LOC254128), transcript variant 3, non-coding RNA [NR_037857]
1690	A_24_P273742	2,128	up	TTC9	Homo sapiens tetratricopeptide repeat domain 9 (TTC9), mRNA [NM_015351]
1691	A_33_P3261982	2,128	up	PRIM2	Homo sapiens primase, DNA, polypeptide 2 (58kDa) (PRIM2), mRNA [NM_000947]
1692	A_33_P3412613	2,128	up	TMPO	Homo sapiens thymopoietin (TMPO), transcript variant 2, mRNA [NM_001032283]
1693	A_33_P3347457	2,127	up		
1694	A_23_P52499	2,127	up	SLC18A2	Homo sapiens solute carrier family 18 (vesicular monoamine), member 2 (SLC18A2), mRNA [NM_003054]
1695	A_33_P3543013	2,127	up	OR5AK4P	Homo sapiens olfactory-like receptor (PJCG3) pseudogene, mRNA sequence, [AF309700]
1696	A_23_P130743	2,125	up	DKKL1	Homo sapiens dickkopf-like 1 (DKKL1), transcript variant 1, mRNA [NM_014419]
1697	A_33_P3283201	2,125	up		Homo sapiens cDNA FLJ45443 fis, clone BRSSN2012157, [AK128779]
1698	A_23_P158708	2,124	up	DCC	Homo sapiens deleted in colorectal carcinoma (DCC), mRNA [NM_005215]
1699	A_23_P379054	2,124	up	CLDN19	Homo sapiens claudin 19 (CLDN19), transcript variant 1, mRNA [NM_148960]
1700	A_33_P3248429	2,124	up	DACT2	dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis) [Source:HGNC Symbol;Acc:21231] [ENST00000366796]
1701	A_33_P3550894	2,123	up	GATA2	Homo sapiens GATA binding protein 2 (GATA2), transcript variant 1, mRNA [NM_001145661]
1702	A_33_P3287310	2,123	up		
1703	A_33_P3265709	2,123	up	OR2Y1	Homo sapiens olfactory receptor, family 2, subfamily Y, member 1 (OR2Y1), mRNA [NM_001001657]
1704	A_23_P433050	2,123	up	RXFP1	Homo sapiens relaxin/insulin-like family peptide receptor 1 (RXFP1), mRNA [NM_021634]
1705	A_33_P3264657	2,123	up	CYP27C1	Homo sapiens cytochrome P450, family 27, subfamily C, polypeptide 1 (CYP27C1), mRNA [NM_001001665]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1706	A_33_P3269976	2,123	up	GAL	galanin prepropeptide [Source:HGNC Symbol;Acc:4114] [ENST00000538401]
1707	A_33_P3214422	2,123	up	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A [Source:HGNC Symbol;Acc:13233] [ENST00000483551]
1708	A_33_P3291939	2,122	up	CNGA3	Homo sapiens cyclic nucleotide gated channel alpha 3 (CNGA3), transcript variant 1, mRNA [NM_001298]
1709	A_33_P3311750	2,122	up	CCDC144A	Homo sapiens coiled-coil domain containing 144A (CCDC144A), mRNA [NM_014695]
1710	A_33_P3332871	2,122	up		601279876F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621930 5', mRNA sequence [BE616696]
1711	A_24_P391918	2,120	up	L3MBTL4	Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), mRNA [NM_173464]
1712	A_33_P3299619	2,120	up	OR1L1	Homo sapiens olfactory receptor, family 1, subfamily L, member 1 (OR1L1), mRNA [NM_001005236]
1713	A_33_P3386681	2,120	up	MS4A13	Homo sapiens membrane-spanning 4-domains, subfamily A, member 13 (MS4A13), transcript variant 1, mRNA [NM_001012417]
1714	A_24_P261470	2,119	up	NRXN2	Homo sapiens neurexin 2 (NRXN2), transcript variant alpha-2, mRNA [NM_138732]
1715	A_33_P3355281	2,119	up	MIOX	Homo sapiens myo-inositol oxygenase (MIOX), mRNA [NM_017584]
1716	A_23_P117387	2,119	up	MIA2	Homo sapiens melanoma inhibitory activity 2 (MIA2), mRNA [NM_054024]
1717	A_33_P3213982	2,119	up	OR13J1	Homo sapiens olfactory receptor, family 13, subfamily J, member 1 (OR13J1), mRNA [NM_001004487]
1718	A_33_P3634554	2,119	up	LOC284108	full-length cDNA clone CS0DB003YF07 of Neuroblastoma Cot 10-normalized of Homo sapiens (human), [CR616125]
1719	A_33_P3370736	2,119	up		Homo sapiens cDNA FLJ46137 fis, clone TESTI2052288, [AK128018]
1720	A_24_P213548	2,119	up	MAN1A2	Homo sapiens mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA [NM_006699]
1721	A_33_P3338392	2,118	up	PRDM15	Homo sapiens PR domain containing 15 (PRDM15), transcript variant 1, mRNA [NM_022115]
1722	A_32_P75902	2,118	up	C16orf73	Homo sapiens chromosome 16 open reading frame 73 (C16orf73), transcript variant 2, mRNA [NM_152764]
1723	A_23_P358195	2,118	up	GOLGA6L10	Homo sapiens golgin A6 family-like 10 (GOLGA6L10), mRNA [NM_001164465]
1724	A_33_P3267651	2,118	up	DZIP3	Homo sapiens DAZ interacting protein 3, zinc finger (DZIP3), mRNA [NM_014648]
1725	A_33_P3281552	2,118	up	RPGR	Homo sapiens retinitis pigmentosa GTPase regulator (RPGR), transcript variant C, mRNA [NM_001034853]
1726	A_33_P3317548	2,118	up	GTF2IRD2B	GTF2I repeat domain containing 2B [Source:HGNC Symbol;Acc:33125] [ENST00000529695]
1727	A_33_P3306659	2,117	up	LOC728254	Homo sapiens mRNA, clone: sF2, from chromosome 5q21-q22, [AB002446]
1728	A_33_P3280796	2,117	up	LMO7	Homo sapiens cDNA FLJ34733 fis, clone MESAN2006953, highly similar to LIM domain only 7 isoform c, [AK092052]
1729	A_33_P3274701	2,116	up		Homo sapiens cDNA FLJ14100 fis, clone MAMMA1000855, [AK024162]
1730	A_32_P187663	2,116	up	ZNF596	Homo sapiens zinc finger protein 596 (ZNF596), transcript variant 1, mRNA [NM_001042416]
1731	A_33_P3339246	2,116	up	LHX8	Homo sapiens LIM homeobox 8 (LHX8), mRNA [NM_001001933]
1732	A_32_P902988	2,115	up	MATN1	Homo sapiens matrilin 1, cartilage matrix protein (MATN1), mRNA [NM_002379]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1733	A_23_P365086	2,115	up	ANKRD5	Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 1, mRNA [NM_022096]
1734	A_23_P323751	2,114	up	FAM83D	Homo sapiens family with sequence similarity 83, member D (FAM83D), mRNA [NM_030919]
1735	A_23_P105730	2,113	up	MDM1	Homo sapiens Mdm1 nuclear protein homolog (mouse) (MDM1), transcript variant 2, mRNA [NM_020128]
1736	A_33_P3380751	2,113	up	ST8SIA1	Homo sapiens ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1 (ST8SIA1), mRNA [NM_003034]
1737	A_33_P3334923	2,113	up	LOC338758	Homo sapiens hypothetical LOC338758 (LOC338758), non-coding RNA [NR_028138]
1738	A_33_P3268378	2,113	up	FAM167A	Homo sapiens family with sequence similarity 167, member A (FAM167A), mRNA [NM_053279]
1739	A_23_P12816	2,113	up	HELLS	Homo sapiens helicase, lymphoid-specific (HELLS), mRNA [NM_018063]
1740	A_23_P94517	2,112	up	DBC1	Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA [NM_014618]
1741	A_33_P3411291	2,112	up	DGKE	Homo sapiens diacylglycerol kinase, epsilon 64kDa (DGKE), mRNA [NM_003647]
1742	A_33_P3356004	2,112	up	UCKL1-AS1	Homo sapiens UCKL1 antisense RNA 1 (non-protein coding) (UCKL1-AS1), antisense RNA [NR_027287]
1743	A_23_P96658	2,112	up	CYorf15B	Homo sapiens chromosome Y open reading frame 15B (CYorf15B), mRNA [NM_032576]
1744	A_23_P348028	2,111	up	IL36A	Homo sapiens interleukin 36, alpha (IL36A), mRNA [NM_014440]
1745	A_23_P325726	2,111	up	ACOT11	Homo sapiens acyl-CoA thioesterase 11 (ACOT11), transcript variant 1, mRNA [NM_015547]
1746	A_23_P162322	2,111	up	WNT10B	Homo sapiens wingless-type MMTV integration site family, member 10B (WNT10B), mRNA [NM_003394]
1747	A_23_P212675	2,111	up	TXNDC6	thioredoxin domain containing 6 [Source:HGNC Symbol;Acc:21343] [ENST00000333911]
1748	A_33_P3237590	2,111	up	LOC728178	full-length cDNA clone XCL0BA001ZD12 of Placenta of Homo sapiens (human), [CR591631]
1749	A_33_P3321070	2,110	up	WNT4	wingless-type MMTV integration site family, member 4 [Source:HGNC Symbol;Acc:12783] [ENST00000374655]
1750	A_23_P20035	2,109	up	GPR146	Homo sapiens G protein-coupled receptor 146 (GPR146), mRNA [NM_138445]
1751	A_33_P3389704	2,109	up	CES1	Homo sapiens carboxylesterase 1 (CES1), transcript variant 3, mRNA [NM_001266]
1752	A_33_P3422103	2,108	up		
1753	A_33_P3239467	2,108	up	C21orf129	Homo sapiens chromosome 21 open reading frame 129 (C21orf129), non-coding RNA [NR_027272]
1754	A_33_P3296975	2,107	up		Homo sapiens cDNA FLJ36034 fis, clone TESTI2017107, highly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4, [AK093353]
1755	A_33_P3372104	2,106	up		
1756	A_33_P3298440	2,106	up	LOC729324	Homo sapiens cDNA FLJ31019 fis, clone HLUNG2000362, [AK055581]
1757	A_33_P3345319	2,105	up	ZFP64	zinc finger protein 64 homolog (mouse) [Source:HGNC Symbol;Acc:15940] [ENST00000395979]
1758	A_33_P3350580	2,105	up		Homo sapiens cDNA FLJ16784 fis, clone CTONG2003764, [AK131548]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1759	A_23_P320216	2,105	up	FAM55D	Homo sapiens family with sequence similarity 55, member D (FAM55D), transcript variant 1, mRNA [NM_001077639]
1760	A_33_P3234540	2,105	up		
1761	A_33_P3246188	2,104	up	C10orf92	Homo sapiens chromosome 10 open reading frame 92 (C10orf92), mRNA [NM_001200049]
1762	A_33_P3241489	2,104	up	LOC100505876	Homo sapiens hypothetical LOC100505876 (LOC100505876), transcript variant 1, non-coding RNA [NR_037879]
1763	A_33_P3384902	2,102	up	OR6X1	Homo sapiens olfactory receptor, family 6, subfamily X, member 1 (OR6X1), mRNA [NM_001005188]
1764	A_33_P3321602	2,101	up	PHACTR4	phosphatase and actin regulator 4 [Source:HGNC Symbol;Acc:25793] [ENST00000373838]
1765	A_33_P3312044	2,100	up		
1766	A_23_P28224	2,100	up	SCN1A	Homo sapiens sodium channel, voltage-gated, type I, alpha subunit (SCN1A), transcript variant 2, mRNA [NM_006920]
1767	A_33_P3283984	2,100	up	AFG3L1P	Homo sapiens AFG3 ATPase family gene 3-like 1 (S, cerevisiae), pseudogene (AFG3L1P), transcript variant 3, non-coding RNA [NR_003228]
1768	A_32_P206735	2,100	up		L22858 AcOrf-91 peptide {Autographa californica nucleopolyhedrovirus} (exp=-1; wgp=0; cg=1), partial (8%) [THC2483664]
1769	A_23_P112086	2,099	up	DEFA5	Homo sapiens defensin, alpha 5, Paneth cell-specific (DEFA5), mRNA [NM_021010]
1770	A_33_P3392374	2,099	up	TTBK1	Homo sapiens tau tubulin kinase 1 (TTBK1), mRNA [NM_032538]
1771	A_23_P134204	2,098	up	FAM71F1	Homo sapiens family with sequence similarity 71, member F1 (FAM71F1), mRNA [NM_032599]
1772	A_33_P3318606	2,098	up	SHC2	Homo sapiens SHC (Src homology 2 domain containing) transforming protein 2, mRNA (cDNA clone IMAGE:4752153), with apparent retained intron, [BC034544]
1773	A_33_P3220047	2,097	up	AKNA	Homo sapiens AT-hook transcription factor (AKNA), mRNA [NM_030767]
1774	A_32_P48466	2,097	up	LCA5L	Homo sapiens Leber congenital amaurosis 5-like (LCA5L), mRNA [NM_152505]
1775	A_33_P3228617	2,097	up	LUZP2	leucine zipper protein 2 [Source:HGNC Symbol;Acc:23206] [ENST00000405855]
1776	A_33_P3325897	2,097	up	MPL	Homo sapiens myeloproliferative leukemia virus oncogene (MPL), mRNA [NM_005373]
1777	A_33_P3250671	2,096	up	TCF7	Homo sapiens transcription factor 7 (T-cell specific, HMG-box) (TCF7), transcript variant 1, mRNA [NM_003202]
1778	A_23_P122068	2,095	up	C1QTNF3	Homo sapiens C1q and tumor necrosis factor related protein 3 (C1QTNF3), transcript variant 2, mRNA [NM_181435]
1779	A_23_P105495	2,095	up	TAS2R14	Homo sapiens taste receptor, type 2, member 14 (TAS2R14), mRNA [NM_023922]
1780	A_33_P3401295	2,094	up	CRCT1	Homo sapiens cysteine-rich C-terminal 1 (CRCT1), mRNA [NM_019060]
1781	A_33_P3279158	2,094	up	NBPF6	Homo sapiens neuroblastoma breakpoint family, member 6 (NBPF6), transcript variant 2, mRNA [NM_001143988]
1782	A_23_P55616	2,094	up	SLC14A1	Homo sapiens solute carrier family 14 (urea transporter), member 1 (Kidd blood group) (SLC14A1), transcript variant 4, mRNA [NM_001146037]
1783	A_33_P3284077	2,093	up	NUP133	Homo sapiens nucleoporin 133kDa (NUP133), mRNA [NM_018230]
1784	A_33_P3249349	2,093	up	PRAME	preferentially expressed antigen in melanoma [Source:HGNC Symbol;Acc:9336] [ENST00000406503]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1785	A_23_P253921	2,093	up	ZNF167	Homo sapiens zinc finger protein 167 (ZNF167), transcript variant 1, mRNA [NM_018651]
1786	A_23_P145841	2,093	up	SOSTDC1	Homo sapiens sclerostin domain containing 1 (SOSTDC1), mRNA [NM_015464]
1787	A_33_P3392802	2,092	up	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa [Source:HGNC Symbol;Acc:11533] [ENST00000402170]
1788	A_24_P354689	2,092	up	SPOCK1	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1 (SPOCK1), mRNA [NM_004598]
1789	A_33_P3260941	2,092	up	FAM168A	Homo sapiens family with sequence similarity 168, member A (FAM168A), mRNA [NM_015159]
1790	A_33_P3249897	2,092	up		
1791	A_33_P3329958	2,091	up	PYY	Homo sapiens peptide YY (PYY), mRNA [NM_004160]
1792	A_33_P3257170	2,091	up	PRR3	proline rich 3 [Source:HGNC Symbol;Acc:21149] [ENST00000461523]
1793	A_23_P376060	2,091	up	IKZF3	Homo sapiens IKAROS family zinc finger 3 (Aiolos) (IKZF3), transcript variant 1, mRNA [NM_012481]
1794	A_33_P3281258	2,091	up		
1795	A_33_P3280502	2,090	up		
1796	A_23_P152234	2,090	up	CMTM2	Homo sapiens CKLF-like MARVEL transmembrane domain containing 2 (CMTM2), transcript variant 1, mRNA [NM_144673]
1797	A_33_P3348395	2,090	up		Uncharacterized protein ENSP00000372125 [Source:UniProtKB/Swiss-Prot;Acc:A6NCN8] [ENST00000382678]
1798	A_24_P401174	2,090	up	KIAA0556	Homo sapiens KIAA0556 (KIAA0556), mRNA [NM_015202]
1799	A_24_P314515	2,089	up	HNF1A-AS1	Homo sapiens HNF1A antisense RNA 1 (non-protein coding) (HNF1A-AS1), non-coding RNA [NR_024345]
1800	A_33_P3341916	2,089	up	C10orf128	chromosome 10 open reading frame 128 [Source:HGNC Symbol;Acc:27274] [ENST00000374149]
1801	A_33_P3234025	2,089	up		chromosome 1 open reading frame 196 [Source:HGNC Symbol;Acc:32336] [ENST00000412667]
1802	A_32_P150086	2,088	up	ANKRD20A5P	Homo sapiens ankyrin repeat domain 20 family, member A5, pseudogene (ANKRD20A5P), non-coding RNA [NR_040113]
1803	A_33_P3325135	2,088	up	ZSCAN23	Homo sapiens zinc finger and SCAN domain containing 23 (ZSCAN23), mRNA [NM_001012455]
1804	A_33_P3243364	2,088	up	ERCC4	Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA [NM_005236]
1805	A_33_P3211098	2,088	up		
1806	A_33_P3377519	2,087	up	HOXA6	homeobox A6 [Source:HGNC Symbol;Acc:5107] [ENST00000222728]
1807	A_23_P82959	2,087	up	FOXH1	Homo sapiens forkhead box H1 (FOXH1), mRNA [NM_003923]
1808	A_32_P787109	2,087	up	DTHD1	Homo sapiens death domain containing 1 (DTHD1), transcript variant 1, mRNA [NM_001170700]
1809	A_33_P3366064	2,087	up	KIAA0889	Homo sapiens KIAA0889 (KIAA0889), transcript variant 2, mRNA [NM_199181]
1810	A_23_P303978	2,086	up	LOC285943	PREDICTED: Homo sapiens hypothetical LOC285943 (LOC285943), miscRNA [XR_108755]
1811	A_32_P485915	2,086	up	SLC9A11	Homo sapiens solute carrier family 9, member 11 (SLC9A11), mRNA [NM_178527]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1812	A_33_P3345708	2,086	up	CREB3L4	Homo sapiens cAMP responsive element binding protein 3-like 4 (CREB3L4), mRNA [NM_130898]
1813	A_33_P3258265	2,086	up	SEMA6C	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C (SEMA6C), transcript variant 2, mRNA [NM_030913]
1814	A_23_P385911	2,086	up	CEP44	Homo sapiens centrosomal protein 44kDa (CEP44), transcript variant 2, mRNA [NM_001145314]
1815	A_23_P327562	2,086	up	LHX9	Homo sapiens LIM homeobox 9 (LHX9), transcript variant 1, mRNA [NM_020204]
1816	A_33_P3263955	2,086	up	LCN10	Homo sapiens lipocalin 10 (LCN10), mRNA [NM_001001712]
1817	A_33_P3281224	2,086	up		
1818	A_32_P184464	2,085	up	ROPN1	Homo sapiens rhophilin associated tail protein 1 (ROPN1), mRNA [NM_017578]
1819	A_33_P3378081	2,085	up	AGBL1	Homo sapiens ATP/GTP binding protein-like 1 (AGBL1), mRNA [NM_152336]
1820	A_23_P323180	2,085	up	HOXD3	Homo sapiens homeobox D3 (HOXD3), mRNA [NM_006898]
1821	A_33_P3419875	2,085	up		
1822	A_33_P3379606	2,084	up	RGS7BP	Homo sapiens regulator of G-protein signaling 7 binding protein (RGS7BP), mRNA [NM_001029875]
1823	A_33_P3420931	2,084	up		
1824	A_33_P3349496	2,084	up		D86966 Start codon is not identified similarto human ZFY protein, {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (3%) [THC2652081]
1825	A_33_P3296348	2,083	up		
1826	A_33_P3423240	2,082	up	FAM21C	family with sequence similarity 21, member C [Source:HGNC Symbol;Acc:23414] [ENST00000374359]
1827	A_33_P3280916	2,082	up	SNHG4	Homo sapiens small nucleolar RNA host gene 4 (non-protein coding) (SNHG4), transcript variant 1, non-coding RNA [NR_003141]
1828	A_33_P3238455	2,082	up	SRSF6	Homo sapiens serine/arginine-rich splicing factor 6 (SRSF6), transcript variant 2, non-coding RNA [NR_034009]
1829	A_23_P394986	2,082	up	CREG2	Homo sapiens cellular repressor of E1A-stimulated genes 2 (CREG2), mRNA [NM_153836]
1830	A_33_P3266489	2,082	up	OR13H1	Homo sapiens olfactory receptor, family 13, subfamily H, member 1 (OR13H1), mRNA [NM_001004486]
1831	A_33_P3215305	2,082	up	ANKRD62	ankyrin repeat domain 62 [Source:HGNC Symbol;Acc:35241] [ENST00000314074]
1832	A_33_P3210399	2,081	up	SLC14A1	Homo sapiens solute carrier family 14 (urea transporter), member 1 (Kidd blood group) (SLC14A1), transcript variant 4, mRNA [NM_001146037]
1833	A_23_P29394	2,081	up	ATP13A4	Homo sapiens ATPase type 13A4 (ATP13A4), mRNA [NM_032279]
1834	A_33_P3338808	2,080	up		
1835	A_33_P3297345	2,080	up	TTC24	Homo sapiens tetratricopeptide repeat domain 24 (TTC24), mRNA [NM_001105669]
1836	A_33_P3264200	2,080	up	EGFEM1P	Homo sapiens EGF-like and EMI domain containing 1, pseudogene (EGFEM1P), non-coding RNA [NR_021485]
1837	A_33_P3406843	2,079	up	LOC442132	Homo sapiens golgin A6 family-like 1 pseudogene (LOC442132), non-coding RNA [NR_033906]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1838	A_23_P57910	2,079	up	RTP3	Homo sapiens receptor (chemosensory) transporter protein 3 (RTP3), mRNA [NM_031440]
1839	A_23_P54692	2,079	up		Homo sapiens cDNA FLJ12547 fis, clone NT2RM4000634, [AK022609]
1840	A_33_P3258324	2,079	up		
1841	A_33_P3288814	2,078	up		
1842	A_33_P3282384	2,077	up	C5orf25	chromosome 5 open reading frame 25 [Source:HGNC Symbol;Acc:24779] [ENST00000377277]
1843	A_33_P3418400	2,077	up	ATG10	Homo sapiens ATG10 autophagy related 10 homolog (S, cerevisiae) (ATG10), transcript variant 3, mRNA [NM_001131028]
1844	A_23_P253958	2,077	up	LRRC17	Homo sapiens leucine rich repeat containing 17 (LRRC17), transcript variant 2, mRNA [NM_005824]
1845	A_33_P3337574	2,076	up	LOC283480	Homo sapiens hypothetical LOC283480 (LOC283480), non-coding RNA [NR_036486]
1846	A_23_P141459	2,076	up	GIP	Homo sapiens gastric inhibitory polypeptide (GIP), mRNA [NM_004123]
1847	A_23_P70448	2,076	up	HIST1H1A	Homo sapiens histone cluster 1, H1a (HIST1H1A), mRNA [NM_005325]
1848	A_23_P431268	2,076	up	PLEKHA6	Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA [NM_014935]
1849	A_33_P3332581	2,074	up	EGFEM1P	Homo sapiens EGF-like and EMI domain containing 1, pseudogene (EGFEM1P), non-coding RNA [NR_021485]
1850	A_24_P326491	2,074	up	MKX	Homo sapiens mohawk homeobox (MKX), transcript variant 1, mRNA [NM_173576]
1851	A_33_P3376031	2,074	up		PREDICTED: Homo sapiens hypothetical LOC100128770 (LOC100128770), miscRNA [XR_109245]
1852	A_23_P341503	2,074	up	C3orf35	Homo sapiens chromosome 3 open reading frame 35 (C3orf35), transcript variant B, mRNA [NM_178339]
1853	A_23_P58862	2,074	up	FAM135A	Homo sapiens family with sequence similarity 135, member A (FAM135A), transcript variant 2, mRNA [NM_020819]
1854	A_24_P13381	2,074	up	TRPV4	Homo sapiens transient receptor potential cation channel, subfamily V, member 4 (TRPV4), transcript variant 2, mRNA [NM_147204]
1855	A_33_P3232334	2,074	up		armadillo repeat containing, X-linked 4 [Source:HGNC Symbol;Acc:28615] [ENST00000430461]
1856	A_33_P3307810	2,073	up	CCDC148	Homo sapiens coiled-coil domain containing 148 (CCDC148), transcript variant 1, mRNA [NM_138803]
1857	A_24_P55225	2,073	up	RSPH9	Homo sapiens radial spoke head 9 homolog (Chlamydomonas) (RSPH9), transcript variant 1, mRNA [NM_152732]
1858	A_24_P404487	2,073	up	ZNF506	Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121), [AL136548]
1859	A_33_P3293925	2,072	up	CXorf36	Homo sapiens chromosome X open reading frame 36 (CXorf36), transcript variant 1, mRNA [NM_176819]
1860	A_33_P3279871	2,072	up	LOC400682	PREDICTED: Homo sapiens zinc finger protein 100-like (LOC400682), mRNA [XM_001726991]
1861	A_23_P143247	2,072	up	TSHZ2	Homo sapiens teashirt zinc finger homeobox 2 (TSHZ2), transcript variant 1, mRNA [NM_173485]
1862	A_33_P3287710	2,072	up	LOC100128292	Homo sapiens hypothetical LOC100128292 (LOC100128292), non-coding RNA [NR_024585]
1863	A_33_P3312519	2,072	up	KPRP	Homo sapiens keratinocyte proline-rich protein (KPRP), mRNA [NM_001025231]
1864	A_33_P3255824	2,072	up		

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1865	A_33_P3351346	2,071	up	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10 [Source:HGNC Symbol;Acc:14103] [ENST00000523711]
1866	A_23_P257355	2,071	up	OTC	Homo sapiens ornithine carbamoyltransferase (OTC), nuclear gene encoding mitochondrial protein, mRNA [NM_000531]
1867	A_23_P62634	2,071	up	RHCE	Homo sapiens Rh blood group, CcEe antigens (RHCE), transcript variant 1, mRNA [NM_020485]
1868	A_33_P3379004	2,071	up		PREDICTED: Homo sapiens hypothetical protein LOC100294005 (LOC100294005), mRNA [XM_002344742]
1869	A_23_P500093	2,070	up	RGS13	Homo sapiens regulator of G-protein signaling 13 (RGS13), transcript variant 1, mRNA [NM_002927]
1870	A_33_P3406370	2,070	up		KB-EST0005989 BPS7 Homo sapiens cDNA, mRNA sequence [DT220905]
1871	A_33_P3357600	2,070	up	TRIM3	Homo sapiens tripartite motif containing 3 (TRIM3), transcript variant 1, mRNA [NM_006458]
1872	A_33_P3420078	2,070	up	LRP11	low density lipoprotein receptor-related protein 11 [Source:HGNC Symbol;Acc:16936] [ENST00000367368]
1873	A_32_P48949	2,070	up	C9orf129	Homo sapiens chromosome 9 open reading frame 129 (C9orf129), mRNA [NM_001098808]
1874	A_24_P353905	2,069	up	MXRA8	Homo sapiens matrix-remodelling associated 8 (MXRA8), mRNA [NM_032348]
1875	A_33_P3220670	2,069	up	LOC644649	BX108667 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGp998I233958, mRNA sequence [BX108667]
1876	A_33_P3336484	2,069	up	NPIP	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA [NM_006985]
1877	A_23_P102607	2,069	up	CHD6	chromodomain helicase DNA binding protein 6 [Source:HGNC Symbol;Acc:19057] [ENST00000373222]
1878	A_24_P135862	2,069	up		
1879	A_23_P79247	2,068	up	PGAP1	Homo sapiens post-GPI attachment to proteins 1 (PGAP1), mRNA [NM_024989]
1880	A_32_P437876	2,068	up	LOC100133315	Homo sapiens transient receptor potential cation channel, subfamily C, member 2-like (LOC100133315), non-coding RNA [NR_029192]
1881	A_33_P3384284	2,067	up	FAM48B1	Homo sapiens family with sequence similarity 48, member B1 (FAM48B1), mRNA [NM_001136234]
1882	A_33_P3250830	2,067	up	C1orf110	chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:28736] [ENST00000367911]
1883	A_33_P3304082	2,067	up		
1884	A_23_P64306	2,066	up	TRIM48	Homo sapiens tripartite motif containing 48 (TRIM48), mRNA [NM_024114]
1885	A_33_P3293187	2,066	up	SLC14A2	Homo sapiens solute carrier family 14 (urea transporter), member 2 (SLC14A2), transcript variant 1, mRNA [NM_007163]
1886	A_33_P3300267	2,066	up	VIT	Homo sapiens vitrin (VIT), transcript variant 1, mRNA [NM_053276]
1887	A_33_P3771741	2,065	up		Homo sapiens cDNA FLJ34909 fis, clone NT2RI2009301, moderately similar to BIFUNCTIONAL METHYLENETETRAHYDROFOLATE DEHYDROGENASE/CYCLOHYDROLASE, MITOCHONDRIAL PRECURSOR, [AK092228]
1888	A_33_P3283863	2,065	up	ODZ1	Homo sapiens odz, odd Oz/ten-m homolog 1 (Drosophila) (ODZ1), transcript variant 1, mRNA [NM_001163278]
1889	A_33_P3237605	2,065	up		
1890	A_23_P315910	2,065	up	TCEB3C	Homo sapiens transcription elongation factor B polypeptide 3C (elongin A3) (TCEB3C), mRNA [NM_145653]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1891	A_33_P3315944	2,065	up	FIGLA	Homo sapiens folliculogenesis specific basic helix-loop-helix (FIGLA), mRNA [NM_001004311]
1892	A_23_P327462	2,065	up	RFX6	Homo sapiens regulatory factor X, 6 (RFX6), mRNA [NM_173560]
1893	A_33_P3338674	2,064	up	CCDC163P	Homo sapiens coiled-coil domain containing 163, pseudogene (CCDC163P), transcript variant 1, non-coding RNA [NR_033298]
1894	A_33_P3268129	2,064	up		chromosome 1 open reading frame 98 [Source:HGNC Symbol;Acc:21901] [ENST00000367356]
1895	A_23_P373464	2,063	up	AFF3	Homo sapiens AF4/FMR2 family, member 3 (AFF3), transcript variant 1, mRNA [NM_002285]
1896	A_33_P3389771	2,063	up	RBMY1B	Homo sapiens RNA binding motif protein, Y-linked, family 1, member B (RBMY1B), mRNA [NM_001006121]
1897	A_24_P865672	2,063	up		full-length cDNA clone CS0CAP008YG08 of Thymus of Homo sapiens (human), [CR595483]
1898	A_33_P3220213	2,063	up	ARMC3	armadillo repeat containing 3 [Source:HGNC Symbol;Acc:30964] [ENST00000376523]
1899	A_33_P3221353	2,062	up	KIAA0564	Homo sapiens KIAA0564 (KIAA0564), transcript variant 2, mRNA [NM_001009814]
1900	A_33_P3365611	2,062	up		basic transcription factor 3-like 4 [Source:HGNC Symbol;Acc:30547] [ENST00000313334]
1901	A_33_P3217147	2,062	up	GPATCH3	Homo sapiens G patch domain containing 3 (GPATCH3), mRNA [NM_022078]
1902	A_24_P115990	2,062	up	AMHR2	Homo sapiens anti-Mullerian hormone receptor, type II (AMHR2), transcript variant 1, mRNA [NM_020547]
1903	A_33_P3254656	2,061	up		ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (14%) [THC2646829]
1904	A_24_P215653	2,061	up	CLEC14A	Homo sapiens C-type lectin domain family 14, member A (CLEC14A), mRNA [NM_175060]
1905	A_33_P3842551	2,060	up	IKZF2	Homo sapiens IKAROS family zinc finger 2 (Helios) (IKZF2), transcript variant 2, mRNA [NM_001079526]
1906	A_33_P3409274	2,060	up		immunoglobulin heavy variable 3-64 [Source:HGNC Symbol;Acc:5617] [ENST00000454421]
1907	A_24_P58488	2,060	up	C2orf73	Homo sapiens chromosome 2 open reading frame 73 (C2orf73), mRNA [NM_001100396]
1908	A_33_P3242548	2,060	up	PRDM5	Homo sapiens PR domain containing 5 (PRDM5), mRNA [NM_018699]
1909	A_23_P10172	2,060	up	PRSS50	Homo sapiens protease, serine, 50 (PRSS50), mRNA [NM_013270]
1910	A_33_P3271470	2,060	up	GREB1L	Homo sapiens growth regulation by estrogen in breast cancer-like (GREB1L), mRNA [NM_001142966]
1911	A_23_P422115	2,060	up	C9orf116	Homo sapiens chromosome 9 open reading frame 116 (C9orf116), transcript variant 1, mRNA [NM_001048265]
1912	A_32_P123514	2,059	up	PABPC4L	Homo sapiens poly(A) binding protein, cytoplasmic 4-like (PABPC4L), mRNA [NM_001114734]
1913	A_33_P3271038	2,059	up	LOC100509399	PREDICTED: Homo sapiens hypothetical protein LOC100509399 (LOC100509399), mRNA [XM_003119592]
1914	A_33_P3423791	2,059	up	GRHL1	Homo sapiens grainyhead-like 1 (Drosophila) (GRHL1), mRNA [NM_198182]
1915	A_23_P380990	2,059	up	CLEC4F	Homo sapiens C-type lectin domain family 4, member F (CLEC4F), mRNA [NM_173535]
1916	A_33_P3333471	2,059	up		Synthetic construct Homo sapiens gateway clone IMAGE:100020926 3' read SCARA3 mRNA, [CU687439]
1917	A_33_P3374678	2,058	up	TMPRSS11D	Homo sapiens transmembrane protease, serine 11D (TMPRSS11D), mRNA [NM_004262]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1918	A_33_P3217609	2,058	up	TBC1D22A	TBC1 domain family, member 22A [Source:HGNC Symbol;Acc:1309] [ENST00000380995]
1919	A_23_P351	2,058	up	EPB41	Homo sapiens erythrocyte membrane protein band 4,1 (elliptocytosis 1, RH-linked) (EPB41), transcript variant 4, mRNA [NM_203342]
1920	A_33_P3305725	2,057	up	LOC730102	Homo sapiens quinone oxidoreductase-like protein 2 pseudogene (LOC730102), non-coding RNA [NR_037167]
1921	A_33_P3316440	2,056	up		Novel protein (KIAA0894)Sorbin and SH3 domain containing 1, isoform CRA_e [Source:UniProtKB/TrEMBL;Acc:Q5T925] [ENST00000371228]
1922	A_33_P3222635	2,056	up	XGPY2	Homo sapiens Xg pseudogene, Y-linked 2 (XGPY2), non-coding RNA [NR_003254]
1923	A_33_P3211608	2,055	up	IL1RL1	interleukin 1 receptor-like 1 [Source:HGNC Symbol;Acc:5998] [ENST00000393393]
1924	A_33_P3359683	2,055	up	IL16	Homo sapiens interleukin 16 (IL16), transcript variant 3, mRNA [NM_001172128]
1925	A_33_P3261428	2,055	up		
1926	A_33_P3251598	2,055	up		
1927	A_33_P3274299	2,055	up	WIPF3	WAS/WASL interacting protein family, member 3 [Source:HGNC Symbol;Acc:22004] [ENST00000409123]
1928	A_33_P3367126	2,054	up	RGNEF	Homo sapiens 190 kDa guanine nucleotide exchange factor (RGNEF), transcript variant 2, mRNA [NM_001177693]
1929	A_23_P257417	2,054	up	C2orf63	Homo sapiens chromosome 2 open reading frame 63 (C2orf63), transcript variant 1, mRNA [NM_152385]
1930	A_33_P3218704	2,054	up	DNAH3	dynein, axonemal, heavy chain 3 [Source:HGNC Symbol;Acc:2949] [ENST00000396036]
1931	A_32_P212802	2,052	up		
1932	A_33_P3359183	2,052	up	AWAT2	Homo sapiens acyl-CoA wax alcohol acyltransferase 2 (AWAT2), mRNA [NM_001002254]
1933	A_33_P3355717	2,052	up		Homo sapiens cDNA FLJ39779 fis, clone SPLEN2001945, [AK097098]
1934	A_33_P3276062	2,051	up		
1935	A_33_P3326812	2,051	up	LOC100130152	Homo sapiens cDNA FLJ45869 fis, clone OCBBF3004908, [AK127768]
1936	A_32_P86245	2,051	up	EFHC1	Homo sapiens EF-hand domain (C-terminal) containing 1 (EFHC1), transcript variant A, mRNA [NM_018100]
1937	A_33_P3223208	2,050	up	CCDC41	Homo sapiens coiled-coil domain containing 41 (CCDC41), transcript variant 1, mRNA [NM_016122]
1938	A_23_P102364	2,050	up	NGEF	Homo sapiens neuronal guanine nucleotide exchange factor (NGEF), transcript variant 1, mRNA [NM_019850]
1939	A_33_P3316088	2,050	up		
1940	A_33_P3338724	2,050	up	LENG9	Homo sapiens leukocyte receptor cluster (LRC) member 9 (LENG9), mRNA [NM_198988]
1941	A_33_P3353866	2,050	up	MOGAT2	Homo sapiens monoacylglycerol O-acyltransferase 2 (MOGAT2), mRNA [NM_025098]
1942	A_33_P3249837	2,049	up		
1943	A_23_P209799	2,048	up	MYO7B	Homo sapiens myosin VIIB (MYO7B), mRNA [NM_001080527]
1944	A_24_P73730	2,048	up	CCDC113	Homo sapiens coiled-coil domain containing 113 (CCDC113), transcript variant 1, mRNA [NM_014157]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1945	A_33_P3365755	2,047	up	SYT2	Homo sapiens synaptotagmin II (SYT2), transcript variant 2, mRNA [NM_001136504]
1946	A_33_P3420043	2,047	up	CSRNP3	Homo sapiens cysteine-serine-rich nuclear protein 3 (CSRNP3), transcript variant 1, mRNA [NM_001172173]
1947	A_23_P32006	2,047	up	OR13D1	Homo sapiens olfactory receptor, family 13, subfamily D, member 1 (OR13D1), mRNA [NM_001004484]
1948	A_23_P108075	2,047	up	SLC7A10	Homo sapiens solute carrier family 7 (neutral amino acid transporter light chain, asc system), member 10 (SLC7A10), mRNA [NM_019849]
1949	A_24_P409800	2,047	up	KCTD16	Homo sapiens potassium channel tetramerisation domain containing 16 (KCTD16), mRNA [NM_020768]
1950	A_33_P3420083	2,046	up	LOC728690	Homo sapiens cDNA FLJ37323 fis, clone BRAMY2018273, [AK094642]
1951	A_33_P3372688	2,046	up	BHLHA9	Homo sapiens basic helix-loop-helix family, member a9 (BHLHA9), mRNA [NM_001164405]
1952	A_33_P3367836	2,046	up		
1953	A_33_P3229276	2,046	up	ZSCAN2	Homo sapiens zinc finger and SCAN domain containing 2 (ZSCAN2), transcript variant 3, mRNA [NM_001007072]
1954	A_23_P129413	2,046	up	DPEP3	Homo sapiens dipeptidase 3 (DPEP3), transcript variant 1, mRNA [NM_022357]
1955	A_24_P238143	2,046	up	LRRC37A2	Homo sapiens leucine rich repeat containing 37, member A2 (LRRC37A2), mRNA [NM_001006607]
1956	A_33_P3248962	2,045	up	LOC100131742	Homo sapiens cDNA FLJ26662 fis, clone MPG02040, [AK130172]
1957	A_33_P3319593	2,045	up	FBXO31	Homo sapiens F-box protein 31 (FBXO31), mRNA [NM_024735]
1958	A_23_P395585	2,045	up	C3orf22	Homo sapiens chromosome 3 open reading frame 22 (C3orf22), mRNA [NM_152533]
1959	A_33_P3322784	2,045	up	NTRK2	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), transcript variant d, mRNA [NM_001018065]
1960	A_33_P3374903	2,045	up		
1961	A_33_P3406530	2,045	up		
1962	A_23_P301984	2,044	up	C8orf48	Homo sapiens chromosome 8 open reading frame 48 (C8orf48), mRNA [NM_001007090]
1963	A_24_P923757	2,043	up	ATF7IP	Homo sapiens activating transcription factor 7 interacting protein (ATF7IP), mRNA [NM_018179]
1964	A_23_P142070	2,043	up	TSPAN16	Homo sapiens tetraspanin 16 (TSPAN16), mRNA [NM_012466]
1965	A_33_P3504002	2,043	up	LOC286186	Homo sapiens hypothetical LOC286186 (LOC286186), non-coding RNA [NR_033893]
1966	A_24_P941896	2,043	up	GRID1	Homo sapiens glutamate receptor, ionotropic, delta 1 (GRID1), mRNA [NM_017551]
1967	A_33_P3215282	2,043	up	TTBK1	Homo sapiens tau tubulin kinase 1 (TTBK1), mRNA [NM_032538]
1968	A_24_P179504	2,043	up	WDR66	Homo sapiens WD repeat domain 66 (WDR66), transcript variant 1, mRNA [NM_144668]
1969	A_23_P69154	2,043	up	FAM198A	Homo sapiens family with sequence similarity 198, member A (FAM198A), mRNA [NM_001129908]
1970	A_33_P3322050	2,042	up	DYRK1A	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 5, mRNA [NM_130438]
1971	A_23_P130811	2,042	up	ZNF536	Homo sapiens zinc finger protein 536 (ZNF536), mRNA [NM_014717]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1972	A_33_P3377100	2,042	up	GHRH	Homo sapiens growth hormone releasing hormone (GHRH), transcript variant 1, mRNA [NM_021081]
1973	A_33_P3415012	2,042	up	KCNA6	Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 6 (KCNA6), mRNA [NM_002235]
1974	A_33_P3323842	2,042	up	BDNF-AS1	Homo sapiens BDNF antisense RNA 1 (non-protein coding) (BDNF-AS1), transcript variant BT2B, non-coding RNA [NR_002832]
1975	A_33_P3418245	2,041	up		
1976	A_33_P3229215	2,041	up	ATP1A1OS	Homo sapiens ATP1A1 opposite strand (ATP1A1OS), transcript variant 3, non-coding RNA [NR_024126]
1977	A_33_P3276019	2,041	up		doublecortin domain containing 2C [Source:HGNC Symbol;Acc:32696] [ENST00000399143]
1978	A_23_P214565	2,040	up	MAS1L	Homo sapiens MAS1 oncogene-like (MAS1L), mRNA [NM_052967]
1979	A_23_P429383	2,040	up	HOXD9	Homo sapiens homeobox D9 (HOXD9), mRNA [NM_014213]
1980	A_24_P215882	2,040	up	ARHGDIG	Homo sapiens Rho GDP dissociation inhibitor (GDI) gamma (ARHGDIG), mRNA [NM_001176]
1981	A_33_P3292297	2,040	up	COPS7B	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis) (COPS7B), mRNA [NM_022730]
1982	A_32_P110016	2,040	up	LOC727869	PREDICTED: Homo sapiens hypothetical LOC727869 (LOC727869), partial miscRNA [XR_111211]
1983	A_33_P3418175	2,040	up	LYNX1	Homo sapiens Ly6/neurotoxin 1 (LYNX1), transcript variant 1, mRNA [NM_023946]
1984	A_33_P3454968	2,040	up	LOC645553	Homo sapiens cDNA clone IMAGE:5478640, partial cds, [BC062328]
1985	A_33_P3210622	2,040	up	ASB13	Homo sapiens ankyrin repeat and SOCS box containing 13 (ASB13), transcript variant 1, mRNA [NM_024701]
1986	A_33_P3290162	2,039	up	ASB18	Homo sapiens ankyrin repeat and SOCS box containing 18 (ASB18), mRNA [NM_212556]
1987	A_33_P3420380	2,039	up	ITIH5	Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 3, mRNA [NM_001001851]
1988	A_33_P3410060	2,038	up	TTLL6	tubulin tyrosine ligase-like family, member 6 [Source:HGNC Symbol;Acc:26664] [ENST00000418322]
1989	A_33_P3578325	2,038	up	SNORD15A	Homo sapiens small nucleolar RNA, C/D box 15A (SNORD15A), small nucleolar RNA [NR_000005]
1990	A_33_P3360087	2,038	up	BBS9	Homo sapiens Bardet-Biedl syndrome 9 (BBS9), transcript variant 1, mRNA [NM_014451]
1991	A_33_P3211229	2,038	up	SLC35F2	Homo sapiens solute carrier family 35, member F2 (SLC35F2), mRNA [NM_017515]
1992	A_33_P3306427	2,038	up	OR1J2	Homo sapiens olfactory receptor, family 1, subfamily J, member 2 (OR1J2), mRNA [NM_054107]
1993	A_24_P303497	2,037	up	MCM9	Homo sapiens minichromosome maintenance complex component 9 (MCM9), transcript variant 1, mRNA [NM_017696]
1994	A_33_P3362331	2,037	up	DEFB130	Homo sapiens defensin, beta 130 (DEFB130), mRNA [NM_001037804]
1995	A_33_P3246293	2,037	up	HBS1L	Homo sapiens HBS1-like (S, cerevisiae) (HBS1L), transcript variant 3, mRNA [NM_001145207]
1996	A_32_P494790	2,037	up		Q6IMH8_MOUSE (Q6IMH8) ADAM4b, partial (10%) [THC2634785]
1997	A_24_P532180	2,036	up	LOC90246	Homo sapiens hypothetical LOC90246 (LOC90246), non-coding RNA [NR_026954]
1998	A_33_P3382324	2,036	up	TPSD1	Homo sapiens tryptase delta 1 (TPSD1), mRNA [NM_012217]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
1999	A_23_P163737	2,036	up	OR2C1	Homo sapiens olfactory receptor, family 2, subfamily C, member 1 (OR2C1), mRNA [NM_012368]
2000	A_33_P3298960	2,035	up	KDELC2	Homo sapiens KDEL (Lys-Asp-Glu-Leu) containing 2 (KDELC2), mRNA [NM_153705]
2001	A_33_P3309201	2,035	up		Homo sapiens cDNA FLJ43761 fis, clone TESTI2048109, [AK125749]
2002	A_33_P3319134	2,035	up	LOC100506191	PREDICTED: Homo sapiens hypothetical protein LOC100506191 (LOC100506191), mRNA [XM_003118995]
2003	A_33_P3334343	2,035	up	HERC2	Homo sapiens hect domain and RLD 2 (HERC2), mRNA [NM_004667]
2004	A_33_P3377609	2,035	up	SPAM1	Homo sapiens sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding) (SPAM1), transcript variant 3, mRNA [NM_001174044]
2005	A_33_P3217731	2,035	up	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) [Source:HGNC Symbol;Acc:11837] [ENST00000376484]
2006	A_23_P500328	2,035	up	DCX	Homo sapiens doublecortin (DCX), transcript variant 1, mRNA [NM_000555]
2007	A_24_P253780	2,035	up	DBF4B	Homo sapiens DBF4 homolog B (S, cerevisiae) (DBF4B), transcript variant 1, mRNA [NM_145663]
2008	A_33_P3877349	2,034	up	LOC440173	Homo sapiens hypothetical LOC440173 (LOC440173), non-coding RNA [NR_027471]
2009	A_33_P3768196	2,034	up	LOC284551	Homo sapiens hypothetical LOC284551 (LOC284551), non-coding RNA [NR_027085]
2010	A_23_P38952	2,034	up	ACER1	Homo sapiens alkaline ceramidase 1 (ACER1), mRNA [NM_133492]
2011	A_33_P3233005	2,033	up	MBTD1	Homo sapiens mbt domain containing 1 (MBTD1), mRNA [NM_017643]
2012	A_33_P3614398	2,033	up	LOC283516	Homo sapiens cDNA FLJ38916 fis, clone NT2NE2008961, [AK096235]
2013	A_33_P3369663	2,033	up	SUN1	Homo sapiens Sad1 and UNC84 domain containing 1 (SUN1), transcript variant 4, mRNA [NM_001171945]
2014	A_33_P3315979	2,033	up	OR4Q3	Homo sapiens olfactory receptor, family 4, subfamily Q, member 3 (OR4Q3), mRNA [NM_172194]
2015	A_33_P3286953	2,033	up	ADAMTS6	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 6 (ADAMTS6), mRNA [NM_197941]
2016	A_23_P81280	2,033	up	BTNL9	Homo sapiens butyrophilin-like 9 (BTNL9), mRNA [NM_152547]
2017	A_23_P150979	2,033	up	MUCL1	Homo sapiens mucin-like 1 (MUCL1), mRNA [NM_058173]
2018	A_23_P325924	2,033	up	FAM59B	Homo sapiens family with sequence similarity 59, member B (FAM59B), transcript variant 2, mRNA [NM_001191033]
2019	A_33_P3709317	2,033	up	SNORA28	Homo sapiens small nucleolar RNA, H/ACA box 28 (SNORA28), small nucleolar RNA [NR_002964]
2020	A_33_P3374076	2,032	up	SEZ6	Homo sapiens seizure related 6 homolog (mouse) (SEZ6), transcript variant 2, mRNA [NM_001098635]
2021	A_33_P3265494	2,032	up	C6orf138	Homo sapiens chromosome 6 open reading frame 138 (C6orf138), transcript variant 1, mRNA [NM_001013732]
2022	A_33_P3308219	2,032	up		
2023	A_33_P3339256	2,031	up		Homo sapiens cDNA FLJ44991 fis, clone BRAWH3008867, [AK126938]
2024	A_33_P3334436	2,031	up		
2025	A_24_P418203	2,031	up	CNTNAP3	Homo sapiens contactin associated protein-like 3 (CNTNAP3), mRNA [NM_033655]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2026	A_33_P3387856	2,030	up	CENPN	Homo sapiens centromere protein N (CENPN), transcript variant 1, mRNA [NM_001100625]
2027	A_33_P3417517	2,030	up	BRD8	Homo sapiens bromodomain containing 8 (BRD8), transcript variant 2, mRNA [NM_139199]
2028	A_23_P218369	2,030	up	CCL14	Homo sapiens chemokine (C-C motif) ligand 14 (CCL14), transcript variant 3, mRNA [NM_032963]
2029	A_33_P3255459	2,030	up	LOC100133461	Homo sapiens hypothetical LOC100133461 (LOC100133461), non-coding RNA [NR_034136]
2030	A_23_P426835	2,029	up	LOC729652	Homo sapiens mRNA; cDNA DKFZp434L055 (from clone DKFZp434L055), [AL834536]
2031	A_33_P3397733	2,029	up	FAM154B	Homo sapiens family with sequence similarity 154, member B (FAM154B), mRNA [NM_001008226]
2032	A_24_P324712	2,029	up	NPC1L1	Homo sapiens NPC1 (Niemann-Pick disease, type C1, gene)-like 1 (NPC1L1), transcript variant 1, mRNA [NM_013389]
2033	A_33_P3271460	2,029	up	GOLGA1	golgin A1 [Source:HGNC Symbol;Acc:4424] [ENST00000373551]
2034	A_33_P3403048	2,029	up		Homo sapiens cDNA FLJ52225 complete cds, moderately similar to S-adenosylmethionine synthetase isoform type-2 (EC 2,5,1,6), [AK294208]
2035	A_23_P60962	2,028	up	MAPK15	Homo sapiens mitogen-activated protein kinase 15 (MAPK15), mRNA [NM_139021]
2036	A_33_P3366493	2,028	up		
2037	A_33_P3290532	2,028	up	LOC255480	Homo sapiens hypothetical LOC255480 (LOC255480), non-coding RNA [NR_038440]
2038	A_33_P3381762	2,028	up		
2039	A_33_P3315470	2,028	up	LOC255167	Homo sapiens hypothetical LOC255167 (LOC255167), non-coding RNA [NR_024424]
2040	A_23_P134851	2,028	up	DOK2	Homo sapiens docking protein 2, 56kDa (DOK2), mRNA [NM_003974]
2041	A_33_P3251582	2,027	up	LRRC16A	Homo sapiens leucine rich repeat containing 16A (LRRC16A), transcript variant 2, mRNA [NM_001173977]
2042	A_33_P3292230	2,027	up	LOC402160	Homo sapiens hypothetical protein LOC402160 (LOC402160), mRNA [NM_001193282]
2043	A_23_P207445	2,027	up	MAP2K6	Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), mRNA [NM_002758]
2044	A_33_P3292646	2,027	up	C10orf112	chromosome 10 open reading frame 112 [Source:HGNC Symbol;Acc:24331] [ENST00000454679]
2045	A_33_P3308307	2,026	up	TMC1	Homo sapiens transmembrane channel-like 1 (TMC1), mRNA [NM_138691]
2046	A_23_P148422	2,026	up	PCYT1B	Homo sapiens phosphate cytidylyltransferase 1, choline, beta (PCYT1B), transcript variant 1, mRNA [NM_004845]
2047	A_23_P345707	2,025	up	C15orf42	Homo sapiens chromosome 15 open reading frame 42 (C15orf42), mRNA [NM_152259]
2048	A_33_P3295348	2,025	up	CLEC2A	Homo sapiens C-type lectin domain family 2, member A (CLEC2A), mRNA [NM_001130711]
2049	A_33_P3322539	2,025	up	BEND2	Homo sapiens BEN domain containing 2 (BEND2), transcript variant 2, mRNA [NM_001184767]
2050	A_33_P3223243	2,025	up	ST7L	suppression of tumorigenicity 7 like [Source:HGNC Symbol;Acc:18441] [ENST00000369664]
2051	A_33_P3264116	2,025	up	NHLRC1	Homo sapiens NHL repeat containing 1 (NHLRC1), mRNA [NM_198586]
2052	A_33_P3261545	2,025	up		Homo sapiens cDNA clone IMAGE:4994693, [BC028053]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2053	A_33_P3392097	2,024	up		
2054	A_33_P3368109	2,024	up		Q6V5H5_9BRAS (Q6V5H5) Pollen coat oleosin-glycine rich protein, partial (13%) [THC2686826]
2055	A_33_P3274501	2,024	up	KLRF1	Homo sapiens killer cell lectin-like receptor subfamily F, member 1 (KLRF1), mRNA [NM_016523]
2056	A_33_P3390823	2,024	up		
2057	A_23_P136777	2,023	up	APOD	Homo sapiens apolipoprotein D (APOD), mRNA [NM_001647]
2058	A_33_P3379712	2,023	up		
2059	A_23_P212354	2,023	up	CCR2	Homo sapiens chemokine (C-C motif) receptor 2 (CCR2), transcript variant A, mRNA [NM_001123041]
2060	A_23_P128008	2,023	up	CCDC81	Homo sapiens coiled-coil domain containing 81 (CCDC81), transcript variant 2, mRNA [NM_021827]
2061	A_24_P323754	2,023	up	LOC100131510	PREDICTED: Homo sapiens hypothetical LOC100131510 (LOC100131510), miscRNA [XR_109960]
2062	A_23_P16354	2,022	up	ZNF382	Homo sapiens zinc finger protein 382 (ZNF382), mRNA [NM_032825]
2063	A_33_P3212394	2,022	up	FRG2C	Homo sapiens FSHD region gene 2 family, member C (FRG2C), mRNA [NM_001124759]
2064	A_32_P206104	2,022	up		
2065	A_23_P337899	2,022	up	MARCH10	Homo sapiens membrane-associated ring finger (C3HC4) 10 (MARCH10), transcript variant 1, mRNA [NM_152598]
2066	A_23_P349463	2,022	up	CHP2	Homo sapiens calcineurin B homologous protein 2 (CHP2), mRNA [NM_022097]
2067	A_23_P67952	2,022	up	MYCNOS	Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) opposite strand (MYCNOS), non-coding RNA [NR_026766]
2068	A_24_P84822	2,022	up	GUSBP1	Homo sapiens glucuronidase, beta pseudogene 1 (GUSBP1), transcript variant 3, non-coding RNA [NR_027028]
2069	A_33_P3230374	2,022	up	OR52I2	Homo sapiens olfactory receptor, family 52, subfamily I, member 2 (OR52I2), mRNA [NM_001005170]
2070	A_33_P3409234	2,021	up		DA399191 BRTHA3 Homo sapiens cDNA clone BRTHA3001578 5', mRNA sequence [DA399191]
2071	A_33_P3365732	2,021	up	TNKS1BP1	Homo sapiens tankyrase 1 binding protein 1, 182kDa (TNKS1BP1), mRNA [NM_033396]
2072	A_33_P3239101	2,021	up	GOLGA6L10	Homo sapiens golgin A6 family-like 10 (GOLGA6L10), mRNA [NM_001164465]
2073	A_33_P3379381	2,020	up	WDR78	Homo sapiens WD repeat domain 78 (WDR78), transcript variant 2, mRNA [NM_207014]
2074	A_33_P3279629	2,020	up	UCN2	Homo sapiens urocortin 2 (UCN2), mRNA [NM_033199]
2075	A_33_P3271530	2,020	up	PGAP1	Homo sapiens post-GPI attachment to proteins 1 (PGAP1), mRNA [NM_024989]
2076	A_24_P237175	2,020	up	CST2	Homo sapiens cystatin SA (CST2), mRNA [NM_001322]
2077	A_24_P129341	2,018	up	AKR1B10	Homo sapiens aldo-keto reductase family 1, member B10 (aldose reductase) (AKR1B10), mRNA [NM_020299]
2078	A_33_P3227857	2,018	up	COX18	Homo sapiens COX18 cytochrome c oxidase assembly homolog (S, cerevisiae) (COX18), nuclear gene encoding mitochondrial protein, mRNA [NM_173827]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2079	A_33_P3354326	2,018	up		
2080	A_33_P3330404	2,018	up	FAM180B	Homo sapiens family with sequence similarity 180, member B (FAM180B), mRNA [NM_001164379]
2081	A_33_P3301955	2,017	up	PDE7A	Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 3, mRNA [NM_001242318]
2082	A_33_P3327462	2,017	up	TMEM108	Homo sapiens transmembrane protein 108 (TMEM108), transcript variant 1, mRNA [NM_023943]
2083	A_23_P318989	2,017	up	C3orf24	Homo sapiens chromosome 3 open reading frame 24 (C3orf24), transcript variant 1, mRNA [NM_173472]
2084	A_23_P6201	2,017	up	LIPI	Homo sapiens lipase, member I (LIPI), mRNA [NM_198996]
2085	A_23_P170901	2,017	up	PACRG	Homo sapiens PARK2 co-regulated (PACRG), transcript variant 1, mRNA [NM_152410]
2086	A_33_P3266993	2,017	up		PREDICTED: Homo sapiens hypothetical protein LOC100506344 (LOC100506344), mRNA [XM_003118742]
2087	A_32_P429687	2,017	up	TRIM72	Homo sapiens tripartite motif containing 72 (TRIM72), mRNA [NM_001008274]
2088	A_33_P3380642	2,017	up	FRAS1	Fraser syndrome 1 [Source:HGNC Symbol;Acc:19185] [ENST00000264899]
2089	A_33_P3410351	2,016	up	GSTM2	Homo sapiens glutathione S-transferase mu 2 (muscle) (GSTM2), transcript variant 1, mRNA [NM_000848]
2090	A_33_P3411307	2,016	up	LOC100130276	Homo sapiens cDNA FLJ46406 fis, clone THYMU3009755, [AK128269]
2091	A_33_P3402086	2,016	up	MERTK	c-mer proto-oncogene tyrosine kinase [Source:HGNC Symbol;Acc:7027] [ENST00000393237]
2092	A_32_P49309	2,016	up	MRO	Homo sapiens maestro (MRO), transcript variant 1, mRNA [NM_031939]
2093	A_33_P3384988	2,015	up	SLC30A5	Homo sapiens solute carrier family 30 (zinc transporter), member 5 (SLC30A5), transcript variant 2, mRNA [NM_024055]
2094	A_23_P396115	2,015	up	SSX7	Homo sapiens synovial sarcoma, X breakpoint 7 (SSX7), mRNA [NM_173358]
2095	A_23_P368067	2,015	up	TAP2	Homo sapiens transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) (TAP2), transcript variant 2, mRNA [NM_018833]
2096	A_33_P3411325	2,015	up		Q8IVL5_HUMAN (Q8IVL5) Leprecan-like 1 protein, partial (3%) [THC2668129]
2097	A_24_P256415	2,014	up	LOC100128288	Homo sapiens hypothetical LOC100128288 (LOC100128288), non-coding RNA [NR_024447]
2098	A_24_P551842	2,014	up	CYTB	mitochondrially encoded cytochrome b [Source:HGNC Symbol;Acc:7427] [ENST00000361789]
2099	A_33_P3301709	2,014	up	GNG4	Homo sapiens guanine nucleotide binding protein (G protein), gamma 4 (GNG4), transcript variant 1, mRNA [NM_001098722]
2100	A_33_P3260733	2,014	up	GHR	Homo sapiens growth hormone receptor (GHR), transcript variant 12, mRNA [NM_001242462]
2101	A_33_P3248774	2,013	up		
2102	A_24_P15877	2,013	up		Homo sapiens FKSG41 (FKSG41) mRNA, complete cds, [AF333762]
2103	A_33_P3353737	2,013	up	ADH1B	Homo sapiens alcohol dehydrogenase 1B (class I), beta polypeptide (ADH1B), mRNA [NM_000668]
2104	A_24_P374244	2,013	up	GATA1	Homo sapiens GATA binding protein 1 (globin transcription factor 1) (GATA1), mRNA [NM_002049]
2105	A_33_P3332052	2,012	up	SLC26A11	Homo sapiens solute carrier family 26, member 11 (SLC26A11), transcript variant 1, mRNA [NM_001166347]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2106	A_33_P3356356	2,012	up	LOC100131089	Homo sapiens hypothetical LOC100131089 (LOC100131089), transcript variant 1, non-coding RNA [NR_040059]
2107	A_33_P3227212	2,012	up		
2108	A_23_P328545	2,012	up	GABRP	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), mRNA [NM_014211]
2109	A_33_P3319886	2,012	up	C19orf45	Homo sapiens chromosome 19 open reading frame 45 (C19orf45), mRNA [NM_198534]
2110	A_33_P3356070	2,012	up	LPIN1	Homo sapiens lipin 1 (LPIN1), mRNA [NM_145693]
2111	A_33_P3220020	2,012	up	LOC440518	Homo sapiens golgin A2 pseudogene (LOC440518), non-coding RNA [NR_033899]
2112	A_33_P3256550	2,011	up	MST152	Homo sapiens MSTP152 (MST152) mRNA, complete cds, [AF190155]
2113	A_23_P15844	2,011	up	BRIP1	Homo sapiens BRCA1 interacting protein C-terminal helicase 1 (BRIP1), mRNA [NM_032043]
2114	A_33_P3268989	2,011	up		ASCC1_HUMAN (Q8N9N2) Activating signal cointegrator 1 complex subunit 1 (ASC-1 complex subunit p50) (Trip4 complex subunit p50), complete [THC2581013]
2115	A_33_P3250173	2,011	up	IQCJ	Homo sapiens IQ motif containing J (IQCJ), transcript variant 1, mRNA [NM_001042705]
2116	A_33_P3399448	2,011	up	SH3TC1	Homo sapiens SH3 domain and tetratricopeptide repeats 1, mRNA (cDNA clone IMAGE:6291103), complete cds, [BC068094]
2117	A_33_P3305536	2,011	up	METTL15	methyltransferase like 15 [Source:HGNC Symbol;Acc:26606] [ENST00000437814]
2118	A_33_P3298634	2,011	up	NFS1	Homo sapiens NFS1 nitrogen fixation 1 homolog (S, cerevisiae) (NFS1), transcript variant 3, mRNA [NM_001198989]
2119	A_33_P3293598	2,011	up	LOC144776	Homo sapiens hypothetical LOC144776 (LOC144776), non-coding RNA [NR_027039]
2120	A_33_P3226610	2,011	up	PSIP1	Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), transcript variant 1, mRNA [NM_021144]
2121	A_33_P3325110	2,011	up	SOX13	Homo sapiens SRY (sex determining region Y)-box 13 (SOX13), mRNA [NM_005686]
2122	A_33_P3341289	2,010	up		
2123	A_24_P21507	2,010	up	SPAG6	Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA [NM_172242]
2124	A_33_P3236642	2,010	up	MIA3	Homo sapiens melanoma inhibitory activity family, member 3 (MIA3), mRNA [NM_198551]
2125	A_32_P790284	2,010	up	KATNAL2	Homo sapiens katanin p60 subunit A-like 2 (KATNAL2), mRNA [NM_031303]
2126	A_33_P3409765	2,010	up	MGAM	maltase-glucoamylase (alpha-glucosidase) [Source:HGNC Symbol;Acc:7043] [ENST00000312952]
2127	A_23_P2006	2,009	up	CNGA4	Homo sapiens cyclic nucleotide gated channel alpha 4 (CNGA4), mRNA [NM_001037329]
2128	A_33_P3254956	2,009	up	DSCR6	Homo sapiens Down syndrome critical region gene 6 (DSCR6), mRNA [NM_018962]
2129	A_33_P3313730	2,009	up	SH3BP2	Homo sapiens SH3-domain binding protein 2 (SH3BP2), transcript variant 4, mRNA [NM_001145855]
2130	A_33_P3420500	2,009	up	ZDHHC20	Homo sapiens zinc finger, DHHC-type containing 20, mRNA (cDNA clone IMAGE:4824131), complete cds, [BC034944]
2131	A_33_P3316169	2,009	up		zinc finger protein 705E [Source:HGNC Symbol;Acc:33203] [ENST00000525199]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2132	A_33_P3387429	2,009	up		
2133	A_33_P3265514	2,009	up	TPTE	Homo sapiens transmembrane phosphatase with tensin homology (TPTE), transcript variant 1, mRNA [NM_199261]
2134	A_32_P377032	2,008	up	C2orf52	Homo sapiens chromosome 2 open reading frame 52 (C2orf52), non-coding RNA [NR_024079]
2135	A_33_P3283083	2,008	up	INPP4B	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), transcript variant 1, mRNA [NM_003866]
2136	A_33_P3271975	2,007	up	LOC100132368	Homo sapiens cDNA FLJ16817 fis, clone TLIVE2007192, [AK131565]
2137	A_24_P393611	2,007	up	GNAO1	Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O (GNAO1), transcript variant 2, mRNA [NM_138736]
2138	A_33_P3300985	2,007	up	LOC731932	PREDICTED: Homo sapiens hypothetical protein LOC731932 (LOC731932), mRNA [XM_001716667]
2139	A_23_P395464	2,007	up	ZNF582	Homo sapiens zinc finger protein 582 (ZNF582), mRNA [NM_144690]
2140	A_33_P3353906	2,007	up		
2141	A_24_P280148	2,006	up	GPR82	Homo sapiens G protein-coupled receptor 82 (GPR82), mRNA [NM_080817]
2142	A_33_P3288434	2,006	up		
2143	A_24_P238543	2,006	up	PHKA1	Homo sapiens phosphorylase kinase, alpha 1 (muscle) (PHKA1), transcript variant 1, mRNA [NM_002637]
2144	A_23_P133075	2,006	up	TBCK	Homo sapiens TBC1 domain containing kinase (TBCK), transcript variant 4, mRNA [NM_033115]
2145	A_33_P3396120	2,006	up	ZNF594	Homo sapiens zinc finger protein 594 (ZNF594), mRNA [NM_032530]
2146	A_24_P283324	2,005	up	ALDH8A1	Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA [NM_022568]
2147	A_33_P3283813	2,005	up	SLC30A8	Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), transcript variant 4, mRNA [NM_001172813]
2148	A_23_P96688	2,005	up	SUV420H1	Homo sapiens suppressor of variegation 4-20 homolog 1 (Drosophila) (SUV420H1), transcript variant 2, mRNA [NM_016028]
2149	A_33_P3242833	2,004	up	PKN2	Homo sapiens protein kinase N2 (PKN2), mRNA [NM_006256]
2150	A_23_P51565	2,004	up	TNNI1	Homo sapiens troponin I type 1 (skeletal, slow) (TNNI1), mRNA [NM_003281]
2151	A_23_P42565	2,002	up	HTR5A	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA [NM_024012]
2152	A_23_P153797	2,002	up	NCAN	Homo sapiens neurocan (NCAN), mRNA [NM_004386]
2153	A_24_P359030	2,002	up	NCRNA00167	Homo sapiens non-protein coding RNA 167 (NCRNA00167), non-coding RNA [NR_024233]
2154	A_33_P3291445	2,001	up	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K [Source:HGNC Symbol;Acc:8965] [ENST00000359130]
2155	A_24_P120109	2,001	up	DHX57	Homo sapiens DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 (DHX57), mRNA [NM_198963]
2156	A_33_P3365200	2,001	up		Novel protein [Source:UniProtKB/TrEMBL;Acc:Q5T6G7] [ENST00000538668]
2157	A_33_P3225397	2,001	up		Q93YZ4_ARATH (Q93YZ4) At2g46910/F14M4,26, partial (3%) [THC2672256]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2158	A_33_P3363340	2,001	up	TMEM212	transmembrane protein 212 [Source:HGNC Symbol;Acc:34295] [ENST00000469981]
2159	A_23_P375372	2,001	up	FGA	Homo sapiens fibrinogen alpha chain (FGA), transcript variant alpha, mRNA [NM_021871]
2160	A_23_P370830	2,001	up	KLHL14	Homo sapiens kelch-like 14 (Drosophila) (KLHL14), mRNA [NM_020805]
2161	A_33_P3290898	2,001	up	CPAMD8	Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), mRNA [NM_015692]
2162	A_33_P3296479	2,000	up	APP	Homo sapiens amyloid beta (A4) precursor protein (APP), transcript variant 10, mRNA [NM_001204303]
2163	A_23_P60259	2,002	down	TMEM38B	Homo sapiens transmembrane protein 38B (TMEM38B), mRNA [NM_018112]
2164	A_33_P3405424	2,005	down	IL4I1	Homo sapiens interleukin 4 induced 1 (IL4I1), transcript variant 2, mRNA [NM_172374]
2165	A_32_P226646	2,005	down	LOC100129781	PREDICTED: Homo sapiens hypothetical LOC100129781, transcript variant 2 (LOC100129781), partial miscRNA [XR_109259]
2166	A_23_P59877	2,007	down	FABP5	Homo sapiens fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA [NM_001444]
2167	A_23_P408955	2,009	down	E2F2	Homo sapiens E2F transcription factor 2 (E2F2), mRNA [NM_004091]
2168	A_33_P3777207	2,012	down	MMEL1	Homo sapiens membrane metallo-endopeptidase-like 1 (MMEL1), mRNA [NM_033467]
2169	A_32_P134209	2,012	down	ACVR2B	Homo sapiens activin A receptor, type IIB (ACVR2B), mRNA [NM_001106]
2170	A_23_P377339	2,013	down	C4orf36	Homo sapiens chromosome 4 open reading frame 36 (C4orf36), mRNA [NM_144645]
2171	A_24_P712562	2,013	down	C17orf67	Homo sapiens chromosome 17 open reading frame 67 (C17orf67), mRNA [NM_001085430]
2172	A_33_P3366391	2,014	down		Homo sapiens cDNA FLJ46155 fis, clone TESTI4001517, [AK128036]
2173	A_24_P759477	2,017	down	ITGB8	Homo sapiens integrin, beta 8 (ITGB8), mRNA [NM_002214]
2174	A_23_P358709	2,020	down	AHRR	Homo sapiens aryl-hydrocarbon receptor repressor (AHRR), transcript variant 1, mRNA [NM_020731]
2175	A_23_P23048	2,020	down	S100A9	Homo sapiens S100 calcium binding protein A9 (S100A9), mRNA [NM_002965]
2176	A_23_P305527	2,021	down	TMC2	Homo sapiens transmembrane channel-like 2 (TMC2), mRNA [NM_080751]
2177	A_33_P3329737	2,021	down		T cell receptor beta variable 19 [Source:HGNC Symbol;Acc:12194] [ENST00000390393]
2178	A_23_P304716	2,023	down	HES2	Homo sapiens hairy and enhancer of split 2 (Drosophila) (HES2), mRNA [NM_019089]
2179	A_23_P306479	2,025	down	LOC100009676	Homo sapiens hypothetical LOC100009676 (LOC100009676), non-coding RNA [NR_024407]
2180	A_23_P205489	2,025	down	SLC7A8	Homo sapiens solute carrier family 7 (amino acid transporter light chain, L system), member 8 (SLC7A8), transcript variant 2, mRNA [NM_182728]
2181	A_23_P13683	2,027	down	ZBTB39	Homo sapiens zinc finger and BTB domain containing 39 (ZBTB39), mRNA [NM_014830]
2182	A_24_P942441	2,029	down	NRXN1	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha2, mRNA [NM_001135659]
2183	A_23_P119222	2,033	down	RETN	Homo sapiens resistin (RETN), transcript variant 1, mRNA [NM_020415]
2184	A_24_P143171	2,034	down	TMEM47	Homo sapiens transmembrane protein 47 (TMEM47), mRNA [NM_031442]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2185	A_33_P3298382	2,034	down		Homo sapiens cDNA clone IMAGE:40134159, [BC127811]
2186	A_33_P3229953	2,035	down	EEF1A2	Homo sapiens eukaryotic translation elongation factor 1 alpha 2 (EEF1A2), mRNA [NM_001958]
2187	A_23_P302302	2,039	down	LOC732275	Homo sapiens hypothetical LOC732275 (LOC732275), non-coding RNA [NR_024406]
2188	A_24_P636882	2,040	down	STK17B	Homo sapiens serine/threonine kinase 17b (STK17B), mRNA [NM_004226]
2189	A_24_P405002	2,042	down	PDIK1L	Homo sapiens PDLIM1 interacting kinase 1 like (PDIK1L), transcript variant 1, mRNA [NM_152835]
2190	A_33_P3281695	2,043	down	NLRP3	Homo sapiens NLR family, pyrin domain containing 3 (NLRP3), transcript variant 1, mRNA [NM_004895]
2191	A_23_P204885	2,043	down	PCDH20	Homo sapiens protocadherin 20 (PCDH20), mRNA [NM_022843]
2192	A_24_P883629	2,046	down	C2orf49	chromosome 2 open reading frame 49 [Source:HGNC Symbol;Acc:28772] [ENST00000258457]
2193	A_33_P3223527	2,048	down		
2194	A_23_P126649	2,048	down	PGBD5	Homo sapiens piggyBac transposable element derived 5 (PGBD5), mRNA [NM_024554]
2195	A_23_P156218	2,048	down	GZMK	Homo sapiens granzyme K (granzyme 3; tryptase II) (GZMK), mRNA [NM_002104]
2196	A_23_P165136	2,049	down	LRRC25	Homo sapiens leucine rich repeat containing 25 (LRRC25), mRNA [NM_145256]
2197	A_23_P68610	2,049	down	TPX2	Homo sapiens TPX2, microtubule-associated, homolog (Xenopus laevis) (TPX2), mRNA [NM_012112]
2198	A_23_P373521	2,049	down	HAND2	Homo sapiens heart and neural crest derivatives expressed 2 (HAND2), mRNA [NM_021973]
2199	A_24_P268123	2,050	down	ST3GAL3	Homo sapiens ST3 beta-galactoside alpha-2,3-sialyltransferase 3 (ST3GAL3), transcript variant 1, mRNA [NM_174963]
2200	A_23_P348146	2,051	down	SLAIN1	Homo sapiens SLAIN motif family, member 1 (SLAIN1), transcript variant 1, mRNA [NM_001040153]
2201	A_24_P370096	2,053	down	ZNF230	Homo sapiens zinc finger protein 230 (ZNF230), mRNA [NM_006300]
2202	A_33_P3369530	2,055	down	MAGI1	Homo sapiens membrane associated guanylate kinase, WW and PDZ domain containing 1 (MAGI1), transcript variant 1, mRNA [NM_015520]
2203	A_33_P3261173	2,055	down	FRAT1	Homo sapiens frequently rearranged in advanced T-cell lymphomas (FRAT1), mRNA [NM_005479]
2204	A_33_P3375710	2,058	down		Q39VP6_GEOMG (Q39VP6) Polysaccharide export protein, partial (6%) [THC2755348]
2205	A_33_P3254555	2,058	down	MCM9	Homo sapiens minichromosome maintenance complex component 9 (MCM9), transcript variant 1, mRNA [NM_017696]
2206	A_24_P413669	2,058	down	PFKFB2	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 (PFKFB2), transcript variant 2, mRNA [NM_001018053]
2207	A_24_P164894	2,058	down	DSCR3	Homo sapiens Down syndrome critical region gene 3 (DSCR3), mRNA [NM_006052]
2208	A_33_P3284711	2,060	down	FBXL19-AS1	Homo sapiens FBXL19 antisense RNA 1 (non-protein coding) (FBXL19-AS1), non-coding RNA [NR_024348]
2209	A_23_P52031	2,060	down	PGM1	Homo sapiens phosphoglucomutase 1 (PGM1), transcript variant 1, mRNA [NM_002633]
2210	A_23_P145569	2,063	down	SLC22A1	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), transcript variant 2, mRNA [NM_153187]
2211	A_33_P3386262	2,063	down	CDT1	Homo sapiens chromatin licensing and DNA replication factor 1 (CDT1), mRNA [NM_030928]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2212	A_23_P717	2,064	down	TMEM206	Homo sapiens transmembrane protein 206 (TMEM206), transcript variant 2, mRNA [NM_018252]
2213	A_33_P3286278	2,065	down	GRN	Homo sapiens granulin (GRN), mRNA [NM_002087]
2214	A_33_P3331021	2,065	down	LOC100129148	Homo sapiens hypothetical LOC100129148 (LOC100129148), non-coding RNA [NR_033999]
2215	A_23_P406350	2,067	down	MFSD3	Homo sapiens major facilitator superfamily domain containing 3 (MFSD3), mRNA [NM_138431]
2216	A_33_P3282241	2,068	down	OR5D16	Homo sapiens olfactory receptor, family 5, subfamily D, member 16 (OR5D16), mRNA [NM_001005496]
2217	A_23_P12554	2,069	down	PKD2L1	Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), mRNA [NM_016112]
2218	A_33_P3405334	2,072	down	GM2A	Homo sapiens GM2 ganglioside activator (GM2A), transcript variant 1, mRNA [NM_000405]
2219	A_23_P31725	2,077	down	BLK	Homo sapiens B lymphoid tyrosine kinase (BLK), mRNA [NM_001715]
2220	A_23_P404091	2,078	down	GRPEL2	Homo sapiens GrpE-like 2, mitochondrial (E, coli) (GRPEL2), nuclear gene encoding mitochondrial protein, mRNA [NM_152407]
2221	A_23_P163402	2,079	down	CYP1A1	Homo sapiens cytochrome P450, family 1, subfamily A, polypeptide 1 (CYP1A1), mRNA [NM_000499]
2222	A_24_P81965	2,084	down	RAP2A	Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), mRNA [NM_021033]
2223	A_23_P73837	2,087	down	TLR8	Homo sapiens toll-like receptor 8 (TLR8), mRNA [NM_138636]
2224	A_24_P276791	2,088	down	LRRC42	Homo sapiens leucine rich repeat containing 42 (LRRC42), mRNA [NM_052940]
2225	A_33_P3356517	2,088	down		
2226	A_23_P331770	2,088	down	USP49	Homo sapiens ubiquitin specific peptidase 49 (USP49), mRNA [NM_018561]
2227	A_23_P218442	2,090	down	CEACAM6	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) (CEACAM6), mRNA [NM_002483]
2228	A_33_P3236748	2,091	down	UNQ9370	PREDICTED: Homo sapiens IFMQ9370 (UNQ9370), miscRNA [XR_111551]
2229	A_23_P123853	2,091	down	CCL19	Homo sapiens chemokine (C-C motif) ligand 19 (CCL19), mRNA [NM_006274]
2230	A_33_P3295071	2,091	down		
2231	A_33_P3380383	2,091	down	TIFAB	Homo sapiens TRAF-interacting protein with forkhead-associated domain, family member B (TIFAB), mRNA [NM_001099221]
2232	A_33_P3439713	2,092	down	LOC283713	Homo sapiens cDNA FLJ37663 fis, clone BRHIP2011120, [AK094982]
2233	A_33_P3254811	2,093	down	C3orf70	Homo sapiens chromosome 3 open reading frame 70 (C3orf70), mRNA [NM_001025266]
2234	A_33_P3274084	2,097	down	RHBDL3	Homo sapiens rhomboid, veinlet-like 3 (Drosophila) (RHBDL3), mRNA [NM_138328]
2235	A_33_P3219475	2,097	down	C9orf30-TMEFF1	Homo sapiens C9orf30-TMEFF1 readthrough (C9orf30-TMEFF1), mRNA [NM_001198812]
2236	A_23_P329573	2,099	down	ITGB2	Homo sapiens integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) (ITGB2), transcript variant 1, mRNA [NM_000211]
2237	A_24_P85775	2,099	down	C1orf38	Homo sapiens chromosome 1 open reading frame 38 (C1orf38), transcript variant 2, mRNA [NM_001039477]
2238	A_33_P3243907	2,100	down	CTSD	Homo sapiens cathepsin D (CTSD), mRNA [NM_001909]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2239	A_23_P144490	2,102	down	DCHS2	Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript variant 1, mRNA [NM_017639]
2240	A_23_P152970	2,103	down	RAPGEFL1	Homo sapiens Rap guanine nucleotide exchange factor (GEF)-like 1 (RAPGEFL1), mRNA [NM_016339]
2241	A_23_P431388	2,104	down	SPOCD1	Homo sapiens SPOC domain containing 1 (SPOCD1), mRNA [NM_144569]
2242	A_23_P347610	2,106	down	HAVCR1	Homo sapiens hepatitis A virus cellular receptor 1 (HAVCR1), transcript variant 1, mRNA [NM_012206]
2243	A_23_P6914	2,110	down	OSBPL11	Homo sapiens oxysterol binding protein-like 11 (OSBPL11), mRNA [NM_022776]
2244	A_32_P72181	2,112	down	LOC647946	Homo sapiens hypothetical LOC647946 (LOC647946), non-coding RNA [NR_024391]
2245	A_23_P43763	2,112	down	PLLP	Homo sapiens plasmolipin (PLLP), mRNA [NM_015993]
2246	A_23_P88331	2,115	down	DLGAP5	Homo sapiens discs, large (Drosophila) homolog-associated protein 5 (DLGAP5), transcript variant 1, mRNA [NM_014750]
2247	A_32_P51848	2,115	down	FAM105A	Homo sapiens family with sequence similarity 105, member A (FAM105A), mRNA [NM_019018]
2248	A_24_P555473	2,117	down	MARCH3	Homo sapiens membrane-associated ring finger (C3HC4) 3 (MARCH3), mRNA [NM_178450]
2249	A_24_P386375	2,118	down	IFNA21	Homo sapiens interferon, alpha 21 (IFNA21), mRNA [NM_002175]
2250	A_33_P3258452	2,119	down	C12orf5	Homo sapiens chromosome 12 open reading frame 5 (C12orf5), mRNA [NM_020375]
2251	A_33_P3306085	2,119	down	RAD51AP2	Homo sapiens RAD51 associated protein 2 (RAD51AP2), mRNA [NM_001099218]
2252	A_24_P21985	2,120	down	FOXJ2	Homo sapiens forkhead box J2 (FOXJ2), mRNA [NM_018416]
2253	A_32_P175739	2,122	down	HK2	Homo sapiens hexokinase 2 (HK2), mRNA [NM_000189]
2254	A_23_P40174	2,126	down	MMP9	Homo sapiens matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA [NM_004994]
2255	A_23_P9883	2,129	down	NLRP3	Homo sapiens NLR family, pyrin domain containing 3 (NLRP3), transcript variant 3, mRNA [NM_001079821]
2256	A_32_P385587	2,129	down	ALAS2	Homo sapiens aminolevulinate, delta-, synthase 2 (ALAS2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_000032]
2257	A_24_P335202	2,129	down	CHRDL2	Homo sapiens chordin-like 2 (CHRDL2), mRNA [NM_015424]
2258	A_23_P252062	2,131	down	PPARG	Homo sapiens peroxisome proliferator-activated receptor gamma (PPARG), transcript variant 3, mRNA [NM_138711]
2259	A_33_P3387781	2,139	down	OR2L1P	Homo sapiens olfactory receptor, family 2, subfamily L, member 1 pseudogene (OR2L1P), non-coding RNA [NR_002145]
2260	A_32_P57810	2,143	down	RNF157	Homo sapiens ring finger protein 157 (RNF157), mRNA [NM_052916]
2261	A_33_P3391175	2,144	down	FLJ44385	Homo sapiens cDNA FLJ44385 fis, clone TRACH3036456, [AK126356]
2262	A_23_P210690	2,149	down	TRIB3	Homo sapiens tribbles homolog 3 (Drosophila) (TRIB3), mRNA [NM_021158]
2263	A_33_P3379081	2,149	down		601191189F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535007 5', mRNA sequence [BE265920]
2264	A_33_P3388192	2,149	down	GTSF1	Homo sapiens gametocyte specific factor 1 (GTSF1), mRNA [NM_144594]
2265	A_23_P46871	2,150	down	SLC29A3	Homo sapiens solute carrier family 29 (nucleoside transporters), member 3 (SLC29A3), transcript variant 1, mRNA [NM_018344]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2266	A_24_P570049	2,157	down	PPARA	Homo sapiens peroxisome proliferator-activated receptor alpha (PPARA), transcript variant 5, mRNA [NM_005036]
2267	A_33_P3305851	2,161	down	SELT	Homo sapiens selenoprotein T (SELT), mRNA [NM_016275]
2268	A_32_P70315	2,161	down	TIMP4	Homo sapiens TIMP metallopeptidase inhibitor 4 (TIMP4), mRNA [NM_003256]
2269	A_33_P3315764	2,161	down	TP53	Homo sapiens tumor protein p53 (TP53), transcript variant 1, mRNA [NM_000546]
2270	A_33_P3352652	2,161	down	OR56A3	Homo sapiens olfactory receptor, family 56, subfamily A, member 3 (OR56A3), mRNA [NM_001003443]
2271	A_33_P3422499	2,164	down		
2272	A_23_P302681	2,165	down	FIGNL1	Homo sapiens fidgetin-like 1 (FIGNL1), transcript variant 1, mRNA [NM_001042762]
2273	A_33_P3280385	2,165	down	COL6A3	Homo sapiens collagen, type VI, alpha 3 (COL6A3), transcript variant 3, mRNA [NM_057165]
2274	A_23_P7313	2,169	down	SPP1	Homo sapiens secreted phosphoprotein 1 (SPP1), transcript variant 1, mRNA [NM_001040058]
2275	A_24_P109214	2,171	down	APOC1	Homo sapiens apolipoprotein C-I (APOC1), mRNA [NM_001645]
2276	A_33_P3214343	2,172	down		Q1W9F5_9CHON (Q1W9F5) NADH dehydrogenase subunit 2, partial (5%) [THC2601170]
2277	A_33_P3223825	2,173	down	SRRM3	Homo sapiens serine/arginine repetitive matrix 3 (SRRM3), mRNA [NM_001110199]
2278	A_24_P202522	2,174	down	AQP4	Homo sapiens aquaporin 4 (AQP4), transcript variant a, mRNA [NM_001650]
2279	A_33_P3374087	2,175	down	RBM44	Homo sapiens RNA binding motif protein 44 (RBM44), mRNA [NM_001080504]
2280	A_23_P57588	2,177	down	GTSE1	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA [NM_016426]
2281	A_23_P19333	2,179	down	TREM1	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), transcript variant 1, mRNA [NM_018643]
2282	A_23_P258570	2,182	down	PSMD10	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 (PSMD10), transcript variant 1, mRNA [NM_002814]
2283	A_33_P3272442	2,183	down	LOC100129195	PREDICTED: Homo sapiens hypothetical LOC100129195 (LOC100129195), partial miscRNA [XR_108694]
2284	A_32_P98927	2,185	down	STAG3L4	Homo sapiens stromal antigen 3-like 4 (STAG3L4), mRNA [NM_022906]
2285	A_33_P3292164	2,186	down	KRTAP9-7	keratin associated protein 9-7 [Source:HGNC Symbol;Acc:18915] [ENST00000391354]
2286	A_23_P200728	2,188	down	FCGR3A	Homo sapiens Fc fragment of IgG, low affinity IIIa, receptor (CD16a) (FCGR3A), transcript variant 1, mRNA [NM_000569]
2287	A_33_P3250055	2,188	down	MAPK12	Homo sapiens cDNA, FLJ98809, [AK308768]
2288	A_23_P34644	2,194	down	FCGR2B	Homo sapiens Fc fragment of IgG, low affinity IIb, receptor (CD32) (FCGR2B), transcript variant 1, mRNA [NM_004001]
2289	A_23_P52311	2,195	down	TAF5	Homo sapiens TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa (TAF5), mRNA [NM_006951]
2290	A_23_P217946	2,199	down	CDH23	Homo sapiens cadherin-related 23 (CDH23), transcript variant 1, mRNA [NM_022124]
2291	A_24_P124624	2,200	down	OLR1	Homo sapiens oxidized low density lipoprotein (lectin-like) receptor 1 (OLR1), transcript variant 1, mRNA [NM_002543]
2292	A_33_P3358923	2,200	down	BTLA	Homo sapiens B and T lymphocyte associated (BTLA), transcript variant 1, mRNA [NM_181780]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2293	A_33_P3338071	2,203	down		
2294	A_33_P3376365	2,206	down	HES2	hairy and enhancer of split 2 (Drosophila) [Source:HGNC Symbol;Acc:16005] [ENST00000377836]
2295	A_33_P3305885	2,206	down	WNK2	Homo sapiens WNK lysine deficient protein kinase 2 (WNK2), mRNA [NM_006648]
2296	A_23_P425681	2,210	down	CCK	Homo sapiens cholecystokinin (CCK), transcript variant 1, mRNA [NM_000729]
2297	A_33_P3416366	2,214	down	CHAF1A	Homo sapiens chromatin assembly factor 1, subunit A (p150) (CHAF1A), mRNA [NM_005483]
2298	A_33_P3332625	2,216	down	PRB1	Homo sapiens proline-rich protein BstNI subfamily 1 (PRB1), transcript variant 3, mRNA [NM_199354]
2299	A_33_P3422035	2,216	down	FXYD5	FXYD domain containing ion transport regulator 5 [Source:HGNC Symbol;Acc:4029] [ENST00000392217]
2300	A_33_P3494109	2,216	down	LOC146795	Homo sapiens cDNA FLJ32815 fis, clone TESTI2002840, [AK057377]
2301	A_33_P3343120	2,216	down	IRF8	Homo sapiens interferon regulatory factor 8 (IRF8), mRNA [NM_002163]
2302	A_23_P46356	2,220	down	TNFAIP8L2	Homo sapiens tumor necrosis factor, alpha-induced protein 8-like 2 (TNFAIP8L2), mRNA [NM_024575]
2303	A_33_P3397399	2,228	down	PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme [Source:HGNC Symbol;Acc:9315] [ENST00000394822]
2304	A_33_P3247320	2,229	down	EMR4P	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 4 pseudogene (EMR4P), non-coding RNA [NR_024075]
2305	A_33_P3293913	2,229	down	BICC1	Homo sapiens bicaudal C homolog 1 (Drosophila) (BICC1), mRNA [NM_001080512]
2306	A_24_P226970	2,232	down	ZNF365	Homo sapiens zinc finger protein 365 (ZNF365), transcript variant A, mRNA [NM_014951]
2307	A_33_P3350703	2,232	down	ERO1LB	Homo sapiens ERO1-like beta (S, cerevisiae) (ERO1LB), mRNA [NM_019891]
2308	A_24_P62659	2,232	down	TSPAN2	Homo sapiens tetraspanin 2 (TSPAN2), mRNA [NM_005725]
2309	A_24_P208998	2,233	down	TRIM23	Homo sapiens tripartite motif containing 23 (TRIM23), transcript variant alpha, mRNA [NM_001656]
2310	A_23_P204246	2,234	down	PHC1	Homo sapiens polyhomeotic homolog 1 (Drosophila) (PHC1), mRNA [NM_004426]
2311	A_33_P3209885	2,239	down	PLXDC1	Homo sapiens plexin domain containing 1 (PLXDC1), mRNA [NM_020405]
2312	A_23_P334263	2,251	down	SENP8	Homo sapiens SUMO/sentrin specific peptidase family member 8 (SENP8), transcript variant 2, mRNA [NM_145204]
2313	A_33_P3300117	2,251	down		
2314	A_33_P3276784	2,252	down		
2315	A_33_P3226080	2,258	down	C17orf87	Homo sapiens chromosome 17 open reading frame 87 (C17orf87), mRNA [NM_207103]
2316	A_23_P133956	2,258	down	KIFC1	Homo sapiens kinesin family member C1 (KIFC1), mRNA [NM_002263]
2317	A_24_P102880	2,268	down	NAV1	Homo sapiens neuron navigator 1 (NAV1), transcript variant 1, mRNA [NM_020443]
2318	A_33_P3396600	2,269	down	KDM4B	Homo sapiens lysine (K)-specific demethylase 4B (KDM4B), mRNA [NM_015015]
2319	A_23_P119478	2,271	down	EBI3	Homo sapiens Epstein-Barr virus induced 3 (EBI3), mRNA [NM_005755]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2320	A_33_P3316456	2,283	down	NPL	Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), transcript variant 2, mRNA [NM_001200050]
2321	A_33_P3474319	2,289	down	SLC37A2	Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 2 (SLC37A2), transcript variant 1, mRNA [NM_198277]
2322	A_23_P14515	2,292	down	ACOT4	Homo sapiens acyl-CoA thioesterase 4 (ACOT4), mRNA [NM_152331]
2323	A_23_P206760	2,295	down	HP	Homo sapiens haptoglobin (HP), transcript variant 1, mRNA [NM_005143]
2324	A_23_P368794	2,297	down	TCERG1L	Homo sapiens transcription elongation regulator 1-like (TCERG1L), mRNA [NM_174937]
2325	A_23_P370162	2,305	down	XRRA1	Homo sapiens X-ray radiation resistance associated 1 (XRRA1), mRNA [NM_182969]
2326	A_33_P3277784	2,305	down	NTNG2	netrin G2 [Source:HGNC Symbol;Acc:14288] [ENST00000372179]
2327	A_23_P209288	2,311	down	CUL3	Homo sapiens cullin 3 (CUL3), mRNA [NM_003590]
2328	A_23_P160800	2,311	down	NR0B2	Homo sapiens nuclear receptor subfamily 0, group B, member 2 (NR0B2), mRNA [NM_021969]
2329	A_23_P214079	2,312	down	SPINK1	Homo sapiens serine peptidase inhibitor, Kazal type 1 (SPINK1), mRNA [NM_003122]
2330	A_24_P330518	2,314	down	CA12	Homo sapiens carbonic anhydrase XII (CA12), transcript variant 1, mRNA [NM_001218]
2331	A_23_P82651	2,317	down	NPTX2	Homo sapiens neuronal pentraxin II (NPTX2), mRNA [NM_002523]
2332	A_23_P145096	2,319	down	PLA2G7	Homo sapiens phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) (PLA2G7), transcript variant 1, mRNA [NM_005084]
2333	A_33_P3338853	2,329	down	LOC401233	Homo sapiens HIV-1 Tat specific factor 1 pseudogene (LOC401233), non-coding RNA [NR_033884]
2334	A_23_P352619	2,331	down	TIFA	Homo sapiens TRAF-interacting protein with forkhead-associated domain (TIFA), mRNA [NM_052864]
2335	A_23_P57277	2,334	down	C21orf7	Homo sapiens chromosome 21 open reading frame 7 (C21orf7), mRNA [NM_020152]
2336	A_23_P103310	2,335	down	S100A7	Homo sapiens S100 calcium binding protein A7 (S100A7), mRNA [NM_002963]
2337	A_24_P921897	2,341	down	HOOK1	Homo sapiens hook homolog 1 (Drosophila) (HOOK1), mRNA [NM_015888]
2338	A_23_P420293	2,341	down	C11orf45	Homo sapiens chromosome 11 open reading frame 45 (C11orf45), mRNA [NM_145013]
2339	A_23_P357207	2,343	down	MRAP2	Homo sapiens melanocortin 2 receptor accessory protein 2 (MRAP2), mRNA [NM_138409]
2340	A_33_P3382538	2,344	down	JRKL	Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA [NM_003772]
2341	A_24_P91566	2,345	down	BMP7	Homo sapiens bone morphogenetic protein 7 (BMP7), mRNA [NM_001719]
2342	A_33_P3317005	2,349	down	SLC11A1	Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 (SLC11A1), mRNA [NM_000578]
2343	A_24_P921321	2,350	down	PTPRJ	Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), transcript variant 1, mRNA [NM_002843]
2344	A_23_P369899	2,351	down	TMEM158	Homo sapiens transmembrane protein 158 (gene/pseudogene) (TMEM158), mRNA [NM_015444]
2345	A_24_P810290	2,352	down	PPAPDC1A	Homo sapiens phosphatidic acid phosphatase type 2 domain containing 1A (PPAPDC1A), mRNA [NM_001030059]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2346	A_33_P3403549	2,362	down	TMEM188	Homo sapiens transmembrane protein 188 (TMEM188), mRNA [NM_153261]
2347	A_23_P420196	2,363	down	SOCS1	Homo sapiens suppressor of cytokine signaling 1 (SOCS1), mRNA [NM_003745]
2348	A_23_P153745	2,366	down	IFI30	Homo sapiens interferon, gamma-inducible protein 30 (IFI30), mRNA [NM_006332]
2349	A_33_P3362008	2,366	down	NPPB	Homo sapiens natriuretic peptide B (NPPB), mRNA [NM_002521]
2350	A_32_P21246	2,367	down	HCG27	Homo sapiens HLA complex group 27 (HCG27), non-coding RNA [NR_026791]
2351	A_23_P204304	2,375	down	PTPRO	Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 1, mRNA [NM_030667]
2352	A_23_P416305	2,379	down	RPL27A	Homo sapiens ribosomal protein L27a (RPL27A), mRNA [NM_000990]
2353	A_23_P94533	2,379	down	CTSL1	Homo sapiens cathepsin L1 (CTSL1), transcript variant 1, mRNA [NM_001912]
2354	A_33_P3414912	2,387	down	NPL	Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), transcript variant 3, mRNA [NM_001200056]
2355	A_32_P123255	2,395	down	ANKRD58	Homo sapiens ankyrin repeat domain 58 (ANKRD58), mRNA [NM_001105576]
2356	A_33_P3294317	2,399	down		
2357	A_23_P256561	2,400	down	TLR6	Homo sapiens toll-like receptor 6 (TLR6), mRNA [NM_006068]
2358	A_24_P827037	2,401	down	LRRC15	Homo sapiens leucine rich repeat containing 15 (LRRC15), transcript variant 2, mRNA [NM_130830]
2359	A_33_P3355821	2,408	down	ZNF273	Homo sapiens zinc finger protein 273 (ZNF273), transcript variant 1, mRNA [NM_021148]
2360	A_24_P216654	2,421	down	SOAT1	Homo sapiens sterol O-acyltransferase 1 (SOAT1), nuclear gene encoding mitochondrial protein, transcript variant 688113, mRNA [NM_003101]
2361	A_33_P3214481	2,422	down	P4HA1	Homo sapiens prolyl 4-hydroxylase, alpha polypeptide I (P4HA1), transcript variant 3, mRNA [NM_001142595]
2362	A_33_P3271684	2,422	down	TMEM236	Homo sapiens transmembrane protein 236 (TMEM236), mRNA [NM_001098844]
2363	A_33_P3399593	2,438	down	CCDC134	Homo sapiens coiled-coil domain containing 134 (CCDC134), mRNA [NM_024821]
2364	A_23_P143526	2,440	down	S100B	Homo sapiens S100 calcium binding protein B (S100B), mRNA [NM_006272]
2365	A_33_P3352578	2,441	down	CLEC4D	Homo sapiens C-type lectin domain family 4, member D (CLEC4D), mRNA [NM_080387]
2366	A_23_P380318	2,445	down	EGR4	Homo sapiens early growth response 4 (EGR4), mRNA [NM_001965]
2367	A_23_P145724	2,446	down	C7orf16	Homo sapiens chromosome 7 open reading frame 16 (C7orf16), transcript variant 1, mRNA [NM_006658]
2368	A_33_P3241511	2,449	down	SERPIND1	Homo sapiens serpin peptidase inhibitor, clade D (heparin cofactor), member 1 (SERPIND1), mRNA [NM_000185]
2369	A_23_P350005	2,455	down	TRIML2	Homo sapiens tripartite motif family-like 2 (TRIML2), mRNA [NM_173553]
2370	A_23_P28042	2,460	down	ZNF737	Homo sapiens zinc finger protein 737 (ZNF737), mRNA [NM_001159293]
2371	A_24_P222655	2,465	down	C1QA	Homo sapiens complement component 1, q subcomponent, A chain (C1QA), mRNA [NM_015991]
2372	A_33_P3232557	2,466	down	DLGAP3	Homo sapiens discs, large (Drosophila) homolog-associated protein 3 (DLGAP3), mRNA [NM_001080418]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2373	A_24_P918032	2,472	down	WHAMMP3	Homo sapiens WAS protein homolog associated with actin, golgi membranes and microtubules pseudogene 3 (WHAMMP3), non-coding RNA [NR_003521]
2374	A_23_P356330	2,473	down	PPPDE2	Homo sapiens PPPDE peptidase domain containing 2 (PPPDE2), mRNA [NM_015704]
2375	A_33_P3372044	2,474	down	TPRG1	Homo sapiens tumor protein p63 regulated 1 (TPRG1), mRNA [NM_198485]
2376	A_23_P218282	2,485	down	ZNF434	Homo sapiens zinc finger protein 434 (ZNF434), mRNA [NM_017810]
2377	A_23_P43369	2,486	down	SIT1	Homo sapiens signaling threshold regulating transmembrane adaptor 1 (SIT1), mRNA [NM_014450]
2378	A_23_P135219	2,489	down	GPR21	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA [NM_005294]
2379	A_24_P419276	2,494	down	ZNF248	Homo sapiens zinc finger protein 248 (ZNF248), mRNA [NM_021045]
2380	A_23_P122216	2,501	down	LOX	Homo sapiens lysyl oxidase (LOX), transcript variant 1, mRNA [NM_002317]
2381	A_23_P256107	2,506	down	HPSE	Homo sapiens heparanase (HPSE), transcript variant 1, mRNA [NM_006665]
2382	A_33_P3311740	2,508	down	ZNF774	Homo sapiens zinc finger protein 774 (ZNF774), mRNA [NM_001004309]
2383	A_24_P203407	2,511	down	FITM2	Homo sapiens fat storage-inducing transmembrane protein 2 (FITM2), mRNA [NM_001080472]
2384	A_23_P138194	2,514	down	NCF2	Homo sapiens neutrophil cytosolic factor 2 (NCF2), transcript variant 1, mRNA [NM_000433]
2385	A_24_P298495	2,523	down	LOC100130744	Homo sapiens clone pp7583 unknown mRNA, [AF289590]
2386	A_33_P3364240	2,532	down	PAEP	Homo sapiens progestagen-associated endometrial protein (PAEP), transcript variant 2, mRNA [NM_002571]
2387	A_24_P191790	2,533	down	TMEM33	Homo sapiens transmembrane protein 33 (TMEM33), mRNA [NM_018126]
2388	A_23_P259663	2,536	down	ZKSCAN5	Homo sapiens zinc finger with KRAB and SCAN domains 5 (ZKSCAN5), transcript variant 1, mRNA [NM_014569]
2389	A_33_P3346716	2,546	down	SMTNL1	smoothelin-like 1 [Source:HGNC Symbol;Acc:32394] [ENST00000457912]
2390	A_33_P3298810	2,558	down	FFAR3	Homo sapiens free fatty acid receptor 3 (FFAR3), mRNA [NM_005304]
2391	A_23_P75769	2,567	down	MS4A4A	Homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MS4A4A), transcript variant 1, mRNA [NM_024021]
2392	A_33_P3219850	2,567	down		Q4RKH8_TETNG (Q4RKH8) Chromosome 21 SCAF15029, whole genome shotgun sequence, partial (4%) [THC2702109]
2393	A_23_P99653	2,574	down		T cell receptor alpha variable 13-2 [Source:HGNC Symbol;Acc:12109] [ENST00000390439]
2394	A_23_P60079	2,577	down	ANGPT2	Homo sapiens angiopoietin 2 (ANGPT2), transcript variant 1, mRNA [NM_001147]
2395	A_33_P3319248	2,578	down	ZNF705G	Homo sapiens zinc finger protein 705G (ZNF705G), mRNA [NM_001164457]
2396	A_24_P365767	2,589	down	CYBB	Homo sapiens cytochrome b-245, beta polypeptide (CYBB), mRNA [NM_000397]
2397	A_23_P426472	2,598	down	ZNF45	Homo sapiens zinc finger protein 45 (ZNF45), mRNA [NM_003425]
2398	A_33_P3247042	2,598	down	FPR3	Homo sapiens formyl peptide receptor 3 (FPR3), mRNA [NM_002030]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2399	A_33_P3247689	2,600	down		
2400	A_23_P151634	2,601	down	SUPT16H	Homo sapiens suppressor of Ty 16 homolog (S, cerevisiae) (SUPT16H), mRNA [NM_007192]
2401	A_23_P137935	2,607	down	MNDA	Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), mRNA [NM_002432]
2402	A_23_P205738	2,610	down	BCL11B	Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript variant 1, mRNA [NM_138576]
2403	A_24_P245379	2,610	down	SERPINB2	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), transcript variant 2, mRNA [NM_002575]
2404	A_33_P3247571	2,618	down	MASP2	Homo sapiens mannan-binding lectin serine peptidase 2 (MASP2), transcript variant 2, mRNA [NM_139208]
2405	A_24_P38754	2,624	down	CISD1	Homo sapiens CDGSH iron sulfur domain 1 (CISD1), mRNA [NM_018464]
2406	A_23_P6293	2,632	down	UBASH3A	Homo sapiens ubiquitin associated and SH3 domain containing A (UBASH3A), transcript variant 1, mRNA [NM_018961]
2407	A_23_P26314	2,632	down	ZNF319	Homo sapiens zinc finger protein 319 (ZNF319), mRNA [NM_020807]
2408	A_24_P98047	2,633	down	SLC16A10	Homo sapiens solute carrier family 16, member 10 (aromatic amino acid transporter) (SLC16A10), mRNA [NM_018593]
2409	A_23_P217269	2,634	down	VSIG4	Homo sapiens V-set and immunoglobulin domain containing 4 (VSIG4), transcript variant 1, mRNA [NM_007268]
2410	A_33_P3346538	2,645	down		
2411	A_23_P130444	2,647	down	ZNF701	Homo sapiens zinc finger protein 701 (ZNF701), transcript variant 2, mRNA [NM_018260]
2412	A_23_P140373	2,659	down	FLVCR2	Homo sapiens feline leukemia virus subgroup C cellular receptor family, member 2 (FLVCR2), transcript variant 1, mRNA [NM_017791]
2413	A_33_P3231156	2,660	down		metallothionein 1C, pseudogene [Source:HGNC Symbol;Acc:7395] [ENST00000379816]
2414	A_33_P3423854	2,663	down	C8B	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA [NM_000066]
2415	A_23_P156390	2,668	down	JAKMIP2	Homo sapiens janus kinase and microtubule interacting protein 2 (JAKMIP2), mRNA [NM_014790]
2416	A_33_P3214550	2,681	down	CXCR2	Homo sapiens chemokine (C-X-C motif) receptor 2 (CXCR2), transcript variant 1, mRNA [NM_001557]
2417	A_33_P3301331	2,689	down	CEACAM3	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 3 (CEACAM3), mRNA [NM_001815]
2418	A_24_P319374	2,701	down	GPA33	Homo sapiens glycoprotein A33 (transmembrane) (GPA33), mRNA [NM_005814]
2419	A_23_P106362	2,706	down	AQP9	Homo sapiens aquaporin 9 (AQP9), mRNA [NM_020980]
2420	A_23_P109913	2,714	down	CXCR6	Homo sapiens chemokine (C-X-C motif) receptor 6 (CXCR6), mRNA [NM_006564]
2421	A_23_P137366	2,720	down	C1QB	Homo sapiens complement component 1, q subcomponent, B chain (C1QB), mRNA [NM_000491]
2422	A_23_P21033	2,729	down	GMPS	Homo sapiens guanine monphosphate synthetase (GMPS), mRNA [NM_003875]
2423	A_33_P3220748	2,741	down		
2424	A_23_P210554	2,748	down	SPATA2	Homo sapiens spermatogenesis associated 2 (SPATA2), transcript variant 1, mRNA [NM_006038]
2425	A_33_P3409649	2,749	down	ADAMTS2	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 2 (ADAMTS2), transcript variant 2, mRNA [NM_021599]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2426	A_24_P355145	2,751	down	DNAJC5B	Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 5 beta (DNAJC5B), mRNA [NM_033105]
2427	A_24_P133488	2,760	down	CDCA4	Homo sapiens cell division cycle associated 4 (CDCA4), transcript variant 1, mRNA [NM_017955]
2428	A_32_P206479	2,768	down	ZNF831	Homo sapiens zinc finger protein 831 (ZNF831), mRNA [NM_178457]
2429	A_23_P94186	2,772	down	LYPD2	Homo sapiens LY6/PLAUR domain containing 2 (LYPD2), mRNA [NM_205545]
2430	A_32_P34920	2,810	down	FOXD1	Homo sapiens forkhead box D1 (FOXD1), mRNA [NM_004472]
2431	A_23_P372946	2,812	down	TM4SF19	Homo sapiens transmembrane 4 L six family member 19 (TM4SF19), transcript variant 1, mRNA [NM_138461]
2432	A_33_P3257784	2,814	down	TSPAN17	Homo sapiens tetraspanin 17 (TSPAN17), transcript variant 1, mRNA [NM_012171]
2433	A_33_P3393408	2,815	down	DECR2	Homo sapiens 2,4-dienoyl CoA reductase 2, peroxisomal (DECR2), mRNA [NM_020664]
2434	A_23_P33723	2,818	down	CD163	Homo sapiens CD163 molecule (CD163), transcript variant 1, mRNA [NM_004244]
2435	A_23_P57155	2,838	down	CHGB	Homo sapiens chromogranin B (secretogranin 1) (CHGB), mRNA [NM_001819]
2436	A_33_P3251801	2,842	down	KLRG2	Homo sapiens killer cell lectin-like receptor subfamily G, member 2 (KLRG2), mRNA [NM_198508]
2437	A_33_P3282075	2,850	down	SP6	Homo sapiens Sp6 transcription factor (SP6), mRNA [NM_199262]
2438	A_24_P188800	2,854	down	MARCH1	Homo sapiens membrane-associated ring finger (C3HC4) 1 (MARCH1), transcript variant 2, mRNA [NM_017923]
2439	A_23_P253791	2,896	down	CAMP	Homo sapiens cathelicidin antimicrobial peptide (CAMP), mRNA [NM_004345]
2440	A_23_P55020	2,901	down	CD300LF	Homo sapiens CD300 molecule-like family member f (CD300LF), mRNA [NM_139018]
2441	A_24_P212024	2,920	down		immunoglobulin kappa variable 1-27 [Source:HGNC Symbol;Acc:5735] [ENST00000498435]
2442	A_33_P3247022	2,921	down	CCNE2	Homo sapiens cyclin E2 (CCNE2), mRNA [NM_057749]
2443	A_23_P208302	2,924	down	APOC2	Homo sapiens apolipoprotein C-II (APOC2), mRNA [NM_000483]
2444	A_24_P339126	2,940	down	PRSS21	Homo sapiens protease, serine, 21 (testisin) (PRSS21), transcript variant 3, mRNA [NM_144957]
2445	A_23_P85240	2,943	down	TLR7	Homo sapiens toll-like receptor 7 (TLR7), mRNA [NM_016562]
2446	A_24_P191312	2,943	down	SLC1A4	Homo sapiens solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4), transcript variant 1, mRNA [NM_003038]
2447	A_23_P218549	2,944	down	EMR3	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 3 (EMR3), mRNA [NM_032571]
2448	A_24_P77082	2,947	down	KMO	Homo sapiens kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO), mRNA [NM_003679]
2449	A_33_P3312119	2,959	down	C6orf99	Homo sapiens chromosome 6 open reading frame 99 (C6orf99), mRNA [NM_001195032]
2450	A_23_P7965	2,960	down	PGC	Homo sapiens progastricsin (pepsinogen C) (PGC), transcript variant 1, mRNA [NM_002630]
2451	A_23_P75283	2,986	down	RBP4	Homo sapiens retinol binding protein 4, plasma (RBP4), mRNA [NM_006744]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2452	A_33_P3235631	3,001	down		immunoglobulin kappa variable 5-2 [Source:HGNC Symbol;Acc:5835] [ENST00000390244]
2453	A_33_P3256680	3,006	down	MFHAS1	Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), mRNA [NM_004225]
2454	A_23_P250516	3,008	down		ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (10%) [THC2604076]
2455	A_33_P3250887	3,010	down	C22orf41	Homo sapiens chromosome 22 open reading frame 41 (C22orf41), mRNA [NM_001123225]
2456	A_23_P55270	3,020	down	CCL18	Homo sapiens chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (CCL18), mRNA [NM_002988]
2457	A_33_P3379326	3,029	down	MSR1	Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AI, mRNA [NM_138715]
2458	A_33_P3236798	3,035	down	SRMS	Homo sapiens src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites (SRMS), mRNA [NM_080823]
2459	A_24_P182929	3,047	down	KCNAB1	Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 2, mRNA [NM_003471]
2460	A_23_P153616	3,065	down	MADCAM1	Homo sapiens mucosal vascular addressin cell adhesion molecule 1 (MADCAM1), transcript variant 1, mRNA [NM_130760]
2461	A_23_P91512	3,106	down	CLDN14	Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA [NM_144492]
2462	A_33_P3387991	3,110	down	CEBPE	Homo sapiens CCAAT/enhancer binding protein (C/EBP), epsilon (CEBPE), mRNA [NM_001805]
2463	A_23_P6381	3,169	down	MN1	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA [NM_002430]
2464	A_33_P3381255	3,171	down	CLEC2A	Homo sapiens clone DNA143292 INPE5792 (UNQ5792) mRNA, complete cds, [AY359126]
2465	A_23_P50697	3,201	down	PSG1	Homo sapiens pregnancy specific beta-1-glycoprotein 1 (PSG1), transcript variant 1, mRNA [NM_006905]
2466	A_24_P282043	3,265	down	ZNF28	Homo sapiens zinc finger protein 28 (ZNF28), transcript variant 1, mRNA [NM_006969]
2467	A_33_P3242503	3,280	down	ZNF365	Homo sapiens zinc finger protein 365 (ZNF365), transcript variant C, mRNA [NM_199451]
2468	A_23_P16953	3,284	down	HTR2B	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2B (HTR2B), mRNA [NM_000867]
2469	A_33_P3216913	3,286	down	ABHD15	Homo sapiens abhydrolase domain containing 15 (ABHD15), mRNA [NM_198147]
2470	A_33_P3367850	3,381	down	CHRM4	Homo sapiens cholinergic receptor, muscarinic 4 (CHRM4), mRNA [NM_000741]
2471	A_33_P3233645	3,442	down	MT1G	Homo sapiens metallothionein 1G (MT1G), mRNA [NM_005950]
2472	A_23_P119835	3,452	down	NLRC4	Homo sapiens NLR family, CARD domain containing 4 (NLRC4), transcript variant 1, mRNA [NM_021209]
2473	A_24_P942493	3,476	down	WSCD1	Homo sapiens WSC domain containing 1 (WSCD1), mRNA [NM_015253]
2474	A_24_P328872	3,481	down	CCT5	Homo sapiens chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA [NM_012073]
2475	A_23_P148088	3,484	down	FGG	Homo sapiens fibrinogen gamma chain (FGG), transcript variant gamma-A, mRNA [NM_000509]
2476	A_23_P12746	3,509	down	MRC1	Homo sapiens mannose receptor, C type 1 (MRC1), mRNA [NM_002438]
2477	A_24_P142503	3,528	down	SLC47A1	Homo sapiens solute carrier family 47, member 1 (SLC47A1), mRNA [NM_018242]
2478	A_23_P146146	3,551	down	ATP6V0D2	Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2 (ATP6V0D2), mRNA [NM_152565]

N	Agilent Probe Name	FC (abs) ([Lp] vs [ctrl])	Regulation	Gene Symbol	Description
2479	A_32_P194264	3,578	down	CHAC2	Homo sapiens ChaC, cation transport regulator homolog 2 (E, coli) (CHAC2), mRNA [NM_001008708]
2480	A_33_P3357397	3,587	down		T cell receptor beta variable 29-1 [Source:HGNC Symbol;Acc:12210] [ENST00000422143]
2481	A_23_P201687	3,594	down	HES2	hairy and enhancer of split 2 (Drosophila) [Source:HGNC Symbol;Acc:16005] [ENST00000377836]
2482	A_33_P3299719	3,633	down	RP1L1	retinitis pigmentosa 1-like 1 [Source:HGNC Symbol;Acc:15946] [ENST00000329335]
2483	A_23_P212854	3,675	down	GYPB	Homo sapiens glycophorin B (MNS blood group) (GYPB), mRNA [NM_002100]
2484	A_23_P253752	3,681	down	FAM54A	Homo sapiens family with sequence similarity 54, member A (FAM54A), transcript variant 2, mRNA [NM_138419]
2485	A_23_P98565	3,757	down	MS4A14	Homo sapiens membrane-spanning 4-domains, subfamily A, member 14 (MS4A14), transcript variant 1, mRNA [NM_032597]
2486	A_24_P234415	3,804	down	STAC	Homo sapiens SH3 and cysteine rich domain (STAC), mRNA [NM_003149]
2487	A_24_P320033	3,818	down	CD80	Homo sapiens CD80 molecule (CD80), mRNA [NM_005191]
2488	A_23_P140928	3,861	down	TMC7	Homo sapiens transmembrane channel-like 7 (TMC7), transcript variant 1, mRNA [NM_024847]
2489	A_23_P101992	3,885	down	MARCO	Homo sapiens macrophage receptor with collagenous structure (MARCO), mRNA [NM_006770]
2490	A_24_P372223	3,901	down	MSR1	Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AI, mRNA [NM_138715]
2491	A_23_P55123	3,950	down	COX10	Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA [NM_001303]
2492	A_23_P8820	3,973	down	FABP4	Homo sapiens fatty acid binding protein 4, adipocyte (FABP4), mRNA [NM_001442]
2493	A_33_P3341851	4,110	down	C4orf21	chromosome 4 open reading frame 21 [Source:HGNC Symbol;Acc:25654] [ENST00000309071]
2494	A_33_P3396404	4,375	down	CLLU1OS	Homo sapiens chronic lymphocytic leukemia up-regulated 1 opposite strand (CLLU1OS), mRNA [NM_001025232]
2495	A_23_P156826	4,495	down	C6orf105	Homo sapiens chromosome 6 open reading frame 105 (C6orf105), transcript variant 2, mRNA [NM_032744]
2496	A_24_P277367	5,909	down	CXCL5	Homo sapiens chemokine (C-X-C motif) ligand 5 (CXCL5), mRNA [NM_002994]
2497	A_23_P94216	6,067	down	LONRF1	Homo sapiens LON peptidase N-terminal domain and ring finger 1 (LONRF1), mRNA [NM_152271]
2498	A_33_P3368313	8,240	down	MT1H	Homo sapiens metallothionein 1H (MT1H), mRNA [NM_005951]
2499	A_23_P154675	20,496	down	SNRPB	Homo sapiens small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB), transcript variant 1, mRNA [NM_198216]